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The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.
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### ALIGNMENTS

Beta-Ala (not group ion agents stability. platelet aggregation inhibitor; guanidino group; amidino New RGD peptide(s) useful as anti:platelet aggregation guanidino or amidino gp. at N-terminal to increase stal H2NC (=NH) NH (CH2) CO. Takiguchi Y; aggregation inhibitor peptide #146 Location/Qualifiers 1 A /label= OTHER /note= "OTHER= I defined)" 'n, 93JP-00186755 94WO-JP000999 Katada ADD95004 standard; peptide; (first entry) CORP STEEL WPI; 1995-060950/08 Hayashi Y, (YAWA ) NIPPON Key Modified-site WO9501371-A1. 22-JUN-1994; 30-JUN-1993; Unidentified 12-JAN-1995 29-JAN-2004 Platelet ADD95004 Sato Y,

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                                                      The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.
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                                            salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.
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The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.
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Takiguchi

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The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.
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       The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.
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2006, 08:47:12 ; Search time 14.5116 Seconds (without alignments) 53.043 Million cell updates/sec 7 May Run on:

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Title: Perfect score: Sequence:

BLOSUM62 ' Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Database

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* H G W 4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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### ALIGNMENTS

SULT 1 2565 phycoerythrin a Species: Gastro Date: 15-Jun-2( Accession: A22; Klotz, A.V.; G Biol. Chem. 2( Biol. Chem. 2( Biol. Chem. 2( Cross-reference Cross-reference Accession: A22; Molecule type: Residues: 1-3 a Cross-reference Alternate name SULT 2 0010 giotensin-conv Alternate name Species: Ficus Date: 15-Jun-2 Accession: P00 Maruyama, S.; I ritle: Angiote Reference numb Accession: P00 Molecule type: Reference numb Accession: P00 Molecule type: Reference numb Accession: P00 Wolecule type: Reference numb Accession: P00 Wolecule type: Residues: 1-3 Cross-referenc Experimental s Keywords: angi Query Match Best Local Sim Matches 0;	Qy 1 X 1
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PMID:2386615
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C;Species: Bothrops insularis (island jararaca)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change
C;Accession: F37196
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin
A;Reference number: A37196; MUID:90351557; PMID:2386615
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C; Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_cl C; Accession: PT0636
R; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A; Fitle: Junctional sequences of fetal T cell receptor beta A; Reference number: PT0509; MUID:91277601; PMID:1711558
A; Accession: PT0636
A; Status: translation not shown
A; Molecule type: mRNA
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C;Species: Gallus gallus (chicken)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001
C;Accession: 150412
R;Mao, P.L.; Beauchemin, M.; Bedard, P.A.
J. Biol. Chem. 268, 8131-8139, 1993
A;Title: Quiescence-dependent activation of the p20
A;Reference number: A46643; MUID:93216790; PMID:846
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A;Cross-references: UNIPARC:UPI000017CE9D
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic
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A;Status: preliminary
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C;Species: Bothrops insularis (island jararaca)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 30-Jun-2001
C;Accession: E37196
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptides A;Reference number: A37196; MUID:90351557; PMID:2386615
A;Accession: E37196
A;Accession: E37196
A;Accession: E37196
A;Cross-references: UNIPARC:UPI0000158403
A;Cross-references: UNIPARC:UPI0000158403
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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PMID:1989490
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Si3894
histidinol dehydrogenase (EC 1.1.1.23) - wild cabbage (fragment)
C; Species: Brassica oleracea (wild cabbage)
C; Species: Brassica oleracea (wild cabbage)
C; Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-J
C; Accession: Si3894
R; Nagai, A.; Scheidegger, A.
Arch. Biochem. Biophys. 284, 127-132, 1991
A; Title: Purification and characterization of histidinol dehydrogens
A; Reference number: Si3894; MUID: 91112783; PMID: 1989490
A; Accession: Si3894
A; Molecule type: protein
A; Residues: 1-3 < NAG>
A; Residues: 1-3 < NAG>
A; Experimental source: var. capitata
C; Keywords: dimer; NAD; oxidoreductase
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TRH-like tripeptide - alfalfa
C;Species: Medicago sativa (alfalfa)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_chang
C;Accession: A43391
C;Accession: A43391
C;Accession: A43391
A;Title: Isolation and structural determination of a novel TRH
A;Reference number: A43391; MUID: 92388092; PMID: 1517203
A;Accession: A43391
A;Molecule type: protein
A;Residues: 1-3 < LAC>
A;Residues: 1-3 < LAC>
C;Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status e
F;3/Modified site: amidated carboxyl end (Pro) #status experim
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S68328
blood cell protein A - Molgula manhattensis (fragment)
C; Species: Molgula manhattensis
C; Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C; Accession: S68328
R; Taylor, S.W.; Ross, M.M.; Waite, J.H.
Arch. Biochem. Biophys. 324, 228-240, 1995
A; Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides A; Reference number: S68325; MUID: 96132650; PMID: 8554314
A; Accession: S68328
A; Molecule type: protein
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C; Accession: PT0622; PT0680; PT0582; PT0673
R; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta A; Reference number: PT0509; MUID:91277601; PMID:1711558
A; Reference number: PT0509; MUID:91277601; PMID:1711558
A; Reference number: PT0509; MUID:91277601; PMID:1711558
A; Reference: PT0622
A; Status: translation not shown
A; Residues: 1-3 < FEE>
A; Cross-references: UNIPARC:UP1000017CEA1
A; Experimental source: newborn thymus, strain BALB/c, clone A; Residues: 1-3 < FEE1>
A; Residues: 1-3 < FEE1>
A; Residues: 1-3 < FEE2>
A; Cross-references: UNIPARC:UP1000017CEA1
A; Experimental source: day 19 fetal thymus, strain BALB/c, C; Keywords: T-cell receptor
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100; PMID:7970703
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C; Species: Mus musculus (house mouse)
C; Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #te.
C; Accession: 178890
R; Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.;
Oncogene 9, 3437-3448, 1994
A; Title: Two distinct protein isoforms are encoded by A; Title: Two distinct protein isoforms are encoded by A; Reference number: 158407; MUID:95060800; PMID:797070
A; Reference number: 158407; MUID:95060800; PMID:797070
A; Reference number: JS 4000; MUID:95060800; PMID:797070
A; Residues: 1-3 < RES>
A; Cross-references: UNIPARC:UPI000011E834; GB:L33339; C; Genetics:
A; Genetics:
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0; Mismatches
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Cross-references: UNIPARC:UPI000017CEA1
Experimental source: day 19 fetal thymus,
Kerwords: T-cell receptor
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C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun
C;Accession: PT0578
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0578
A;Accession: PT0578
A;Accession: Chown
A;Molecule type: mRNA
A;Residues: 1-3 <FEE>
A;Cross-references: UNIPARC:UPI000017CE9F
A;Experimental source: day 19 fetal thymus, strain BALB/C
C;Keywords: T-cell receptor
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PT0571
T-cell receptor beta chain.V-D-J region (141-1CM) - mouse (fragment T-cell receptor beta chain.V-D-J region (141-1CM) - mouse (fragment C; Species: Mus musculus (house mouse)
C; Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-C; Accession: PT0571
R; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains. A; Reference number: PT0509; MUID:91277601; PMID:1711558
A; Accession: PT0571
A; Residues: 1-3 < FBE>
Cross-references: UNIPARC:UP1000017CEA0
A; Experimental source: day 19 fetal thymus, strain BALB/c
C; Keywords: T-cell receptor
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PT0622
T-cell receptor beta chain V-D-J region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_c
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                                                         strain BALB/c
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             A;Residues: 1-3 <FEE>
A;Cross-references: UNIPARC:UPI000017CE9E
A;Experimental source: newborn thymus, st:
C;Keywords: T-cell receptor
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A;Residues: 1-3 <TAY> A;Cross-references: UNIPARC:UPI000017CEA2

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C;Species: mitochondrion Lampetra fluviatilis (river lamprey)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2007;Accession: T13892
R;Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.
R;Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A;Title: The main features of the craniate mitochondrial DNA between the A;Reference number: Z17775; MUID:97398704; PMID:9254918
A;Reference number: Z17775; MUID:97398704; PMID:9254918
A;Residues: DNA
A;Residues: 1-3 <DEL>
A;Cross-references: UNIPARC:UPI000011E981; EMBL:Y09528; NID:92340016; PII
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase
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growth-modulating peptide - human

C;Species: Homo sapiens (man)

C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Ma

C;Accession: A01421

R;Schlesinger, D.H.; Pickart, L.; Thaler, M.M.

Experientia 33, 324-325, 1977

A;Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine

A;Reference number: A01421; MUID: 77162369; PMID:858356

A;Reference number: A01421

A;Molecule type: protein

A;Residues: 1-3 <SCH>

A;Residues: 1-3 <SCH>

A;Residues: 1-3 scrum tripeptide is found to stimulate growth of some ce
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2, 2006, 08:38:27 ; Search time 90.6047 Seconds (without alignments) 62.295 Million cell updates/sec using sw model - protein search, May OM protein Run on:

US-10-046-922-32 0 1 XXXXXXXX 8 score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Title: Perfect so Sequence:

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

ription	sepia offi	homo sap	2 vibrio fis	0 bombina o	1 notophth	8 sns sc	Φ	4 ac	ed 9	8 pseudomon	1 homo sa	2 hirudo		5 an	<b>,</b> C;	7 hirudo	L	helisom	7 hirudo med	5 macroca	46 nereis	06 anthopleu	68 sepia off	48 octopus m	49 octopus m	65 pandinus	64 pandinus	58 homo	15 saccharom	47 homo sapi	t0 homo sapien
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MEDLINE=91072226; PubMed=2254256;
Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
"A new Vibrio fischeri lux gene precedes a bidirectional termination
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                                                                                                                                    in vitro.
                                                               PROTEIN SEQUENCE.
MEDLINE=77162369; PubMed=858356;
Schlesinger D.H., Pickart L., Thaler M.M.;
"Growth-modulating serum tripeptide is glycyl-histidyl-lysine."
Experientia 33:324-325(1977).
-:- MISCELLANEOUS: This serum tripeptide has been found to stimi growth of some cell types and to inhibit other types in viti
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Bacteriol. 172:6797-6802(1990).

FUNCTION: Acyl-protein synthetase activates tetradecanoic acid is a component of the fatty acid reductase complex responsible converting tetradecanoic acid to the aldehyde which serves substrate in the luciferase-catalyzed reaction.

CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphospl
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Primates; Catarrhini;
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Vibrionaceae; Vibrio.
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01-MAR-1992 (Rel. 21, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Long-chain-fatty-acid--luciferin-component ligase (EC protein synthetase) (Fragment).
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n: Mismatches
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Euarchontoglires; P:
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P62970; P01151;
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Thyroliberin (Thyrotropin releasing hormone) (TRH) (Thyrotropin releasing factor) (Protirelin).
Bombina orientalis (Oriental fire-bellied toad).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
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DT 21-JUL-1986 (Rel. 45, Last annotation update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

Thyroliberin (Thyrotropin releasing factor)

Thyroliberin (Thyrotropin releasing factor)

Thyroliberin (Thyrotropin releasing factor)

OC Notophthalmus viridescens (Eastern newt) (Triturus viridescens).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;

OC Notophthalmus.

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MEDLINE=76138399; PubMed=815011;
Yasuhara T., Nakajima T.;
"Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
"Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
Chem. Pharm. Bull. 23:3301-3303(1975).
-:- FUNCTION: TRH functions as a regulator of the biosynthesis of in the anterior pituitary gland and as a neurotransmitter/neuromodulator in the central and peripheral nervous systems
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MOD_RES 3 3 Proline amide.
SEQUENCE 3 AA; 380 MW; 7761F6B00000000 CRC64;
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neuromodulator in the central and peripheral nervous system
SUBCELLULAR LOCATION: Secreted.
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1 Pyrrolidone carboxylic acid.

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380 MW; 7761F6B00000000 CRC64;
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Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;
"The identity of chemical and hormonal properties of the thyrot
releasing hormone and pyroglutamyl-histidyl-proline amide.";
Biochem. Biophys. Res. Commun. 37:705-710(1969).

-!- FUNCTION: TRH functions as a regulator of the biosynthesis
in the anterior pituitary gland and as a neurotransmitter/
neuromodulator in the central and peripheral nervous syster
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21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Thyroliberin (Thyrotropin releasing hormone) (TRH) (Tlyroliberin (TRH-releasing factor) (Protirelin)
Releasing factor) (TSH-releasing factor) (Protirelin)
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 TISSUE=Brain;
MEDLINE=75035605; PubMed=4214528;
Grimm-Joergensen Y., McKelvy J.F.;
"Biosynthesis of thyrotropin releasing fa
viridescens) brain in vitro. Isolation an
thyrotropin releasing factor.";
J. Neurochem. 23:471-478(1974).
-!- FUNCTION: TRH functions as a regulato
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MEDLINE=70136150; PubMed=4984938;
Nair R.M.G., Barrett J.F., Bowers
"Structure of porcine thyrotropin
Biochemistry 9:1103-1106(1970)
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Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Caprinae, Ovis.
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ation; Direct protein sequencing; Pyrrolidone carboxylic RES 1 1 Pyrrolidone carboxylic acid.
RES 3 3 Proline amide.
RES 3 3 7761F6B0000000 CRC64;
protein sequencing; Pyrrolidone carboxylic

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Thyroliberin (Thyrotropin releasing hormone) (TRH) (Try releasing factor) (TSH-releasing factor)
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Burgus R., Dunn T.F., Desiderio D.M.,
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Nature 226:321-325(1970)
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TISSUE=Hypothalamus;
Desiderio D.M. Jr.,
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P62969; P01151;
21-JUL-1986 (Rel
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Guillemin R.;
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Bacteria; Proteobacteria; Alphaproteobacteria;
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05-JUL-2004 (Rel. 44, Last annotation update)
Carbon monoxide dehydrogenase small chain (EC dehydrogenase subunit S) (CO-DH S) (Fragment).
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Kraut M., Hugendieck I., Herwig S., Me "Homology and distribution of CO dehyd carboxydotrophic bacteria.";
Arch. Microbiol. 152:335-341(1989).
                                                                                                 Kraut M., Hugendieck I., Herwig S., Me "Homology and distribution of CO dehycarboxydotrophic bacteria.";
Arch. Microbiol. 152:335-341(1989).
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FUNCTION: Neuroexcitatory peptide; increases the impulse frequency and produces a spike broadening of the identified heart excitatory neuron (PON); also enhances the amplitude and frequency of the heart beat. Has also an effect on several other muscles.
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                                                                                                         Pulmonata; Stylommatophora;
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STRAIN=Ferussac; TISSUE=Ganglion;
MEDLINE=89273551; PubMed=2597281;
Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K., Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
"Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica Ferussac containing a D-amino acid residue.";
Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
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Sigmurethra; Achatinoidea; Achatinidae; Achatina
NCBI_TaxID=6530;
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D-amino acid; Direct protein sequencing; Hormone MOD_RES 2 2 D-phenylalanine.
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Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
-!- MISCELLANEOUS: These peptides are released from mast cells in cand other tissues) during hypersensitivity reactions (and other tissues) during hypersensitivity affecting (anaphylaxis). Their activities, preferentially affecting (anaphylaxis). Their activities, chemotactic deactivation, releasinophils, include chemotaxis, chemotactic deactivation, releasinophils, include chemotaxis.
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MEDLINE=76078412; PubMed=1060093;
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MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N,
Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
"Identification of RFamide neuropeptides in the medicinal leech.";
Peptides 12:897-908(1991).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
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01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
FMRFamide-like neuropeptide YMRF-amide.
Hirudo medicinalis (Medicinal leech).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
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MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)
Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
"Identification of RFamide neuropeptides in the medicinal le Peptides 12:897-908(1991).
-! SUBCELLULAR LOCATION: Secreted.
-! SIMILARITY: Belongs to the FARP (FMRFamide related pept:
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Hirudo medicinalis (Medicinal leech).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
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MEDLINE=94286417; PubMed=7912428; DOI=10.1016/0196-9781(94)9016
Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A
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MEDLINE=92028852; PubMed=1681803;
Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
"Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-Kaamide), novel neuropeptide from sea anemones.";
Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
                                                                                                                                                      Zoantharia; Actiniaria;
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MCFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.
"The expansion behaviour of sea anemones may be coordinated by inhibitory neuropeptides, Antho-KAamide and Antho-Rlamide.";
Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
-!- FUNCTION: Inhibits spontaneous contractions in several musc groups. May be involved in the expansion phase of feeding behaviour in sea anemones.
-!- SUBCELLULAR LOCATION: Secreted.
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PROTEIN SEQUENCE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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US-07-820-154A-12
US-07-820-154A-12
Sequence 12, Application US/07820154A
Patent No. 5382425
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES:
ADDRESSEE: John P. White
STREET: 30 Rockefeller.Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820,154A
FILING DATE: 19920113
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
US-08-801-092-10
US-08-801-092-17
US-08-801-092-24
US-08-801-092-31
US-08-801-092-45
US-09-298-017-23
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US-09-298-017-25
US-09-392-979A-25
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US-09-117-927-5
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US-09-315-313-10
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LENGTH: 1 amino acids
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INFORMATION FOR SE
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US-08-293-150A-40

US-08-293-150A-24

US-08-496-847-23

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US-08-742-774-25

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NAME: Warren M. Cheek, REGISTRATION NUMBER: 3
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GY: linear
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                                                                                                                                                                                                                                             COUNTRY: United States

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/791,213D

FILING DATE: 13-NOV-1991

CLASSIFICATION DATA:

APPLICATION NUMBER: JP 2-306745

FILING DATE: 13-NOV-1990

ATTORNEY/AGENT INFORMATION:

NAME: Meuth, Donna M

REGISTRATION NUMBER: 36,607

REFERENCE/DOCKET NUMBER: 029650-032

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECHONE: (703) 836-6620

TELEFAX: (703) 836-2021
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24, Application US/07791213D . 5409895
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APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE,
TITLE OF INVENTION: SAME AND PRO
TITLE OF INVENTION: INHIBITION PITTLE OF INVENTION: TREATING USI
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                                               MORISHITA, Hideaki
KANAMORI, Toshinori
NOBUHARA, Masahiro
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TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO:
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                                         APPLICANT: MORISHITA, H
APPLICANT: KANAMORI, TO
APPLICANT: NOBUHARA, MA
TITLE OF INVENTION: POL
TITLE OF INVENTION: SAM
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TITLE OF INVENTION: INH
TITLE OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS
ADDRESSEE: Burns, Do
                                                                                                                                                                                              STREET: P.O. Box 1
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                         Burns,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T: P.O. Box
Alexandria
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United
   Sequence 24, Applicat
Patent No. 5409895
GENERAL INFORMATION:
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TYPE:
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US-07-791-213D-24
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VENTION: 4-THIAHEPTANOIC ACID DERIVATIVES
EQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144
COMPUTER: IBM Compatible
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W.. CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 57, Application US/08174365A; Patent No. 5478809; GENERAL INFORMATION:
APPLICANT: Seiichi TANIDA et al.
TITLE OF INVENTION: 4-THIAHEPTANOIC; NUMBER OF SEQUENCES: 106; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                         PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-0
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-5620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/(FILING DATE: December 28 CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION
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Bowersox, Stephen S
Fox, James A.
Valentino, Karen L.
Bitner, Robert S.
Yamashiro, Donald H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
FORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                          Nans;
                                                                     Similarity 0.0%; 0; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           Law Offices
                                                                                                                                                                                                                                                                                                                 APPLICANT: Bitner, Rober APPLICANT: Yamashiro, DC TITLE OF INVENTION: Dela TITLE OF INVENTION: ISCH NUMBER OF SEQUENCES: 28 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERISTICS
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NO
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US-07-789-913-25
ORIGINAL SOURCE: INDIVIDUAL ISOLATE:
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HYPOTHETICAL:
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US-07-789-913-23
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CITY: P
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Best Local S
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                                                                                                        LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note = "Xaa is modified amino acid
OTHER INFORMATION: described in specification"
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                                                                                                                                                                                            Length 1;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,913
FILING DATE: 19911112
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/440,094
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TITLE OF INVENTION: Delayed Treatment Method o
TITLE OF INVENTION: Ischemia-Related Neuronal
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
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                                                                                                                                                                                            score 0; DB 1; Pred. No. 0; 0; Mismatches
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R: 5865-0005.30
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ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0005.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                    RESULT 5
US-07-789-913-23
; Sequence 23, Application US/07789913
; Patent No: 5559095
; GENERAL INFORMATION:
; APPLICANT: Miljanich, George P.
; APPLICANT: Bowersox, Stephen S.
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Valentino, Karen L.
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INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: AMINO ACID
TOPOLOGY
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                                                                                           modified site
                                                                                                                                                                                                         Similarity 100
1; Conservative
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NO
       CHARACTERISTICS
                LENGTH: 1 amino acid
TYPE: amino acid
STRANDEDNESS: single
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                                                               linear
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                                                                                                                                                                  US-08-174-365A-57
                                                                                       NAME/KEY:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                               TOPOLOGY:
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CITY: Pa
STATE: C
       SEQUENCE CI
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Length
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                                                                                                                                                                                                                                                                                                  Ischemia-Related Neuronal
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<del>ب</del>
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Avenue, Suite 300
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Mismatches
                            Mismatches
DB
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R: 5865-0005.30
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FILING DATE: 19911112
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-AUG-1990
PRIOR APPLICATION DATA:
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/440,094
FILING DATE: 22-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
  Score
Pred. N
                                                                                                                                                         Sequence 25, Application US/07789913
Patent No. 5559095
GENERAL INFORMATION:
APPLICANT: Miljanich, George P.
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Palo Alto
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RESULT
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                                                                              APPLICANT: SINGH, TEJINDER
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1;
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                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: Patentin PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/049,794

FILING DATE: 19930415
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                                                                                                                                                                                           NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
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US-08-049-794-25

; Sequence 25, Application US/08049794

; Patent No. 5587454

; GENERAL INFORMATION:

; APPLICANT: JUSTICE, ALAN

; APPLICANT: SINGH, TEJINDER

; APPLICANT: GOHIL, KISHOR C

; APPLICANT: VALENTINO, KAREN L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
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0; Mi
                               23, Application US/08049794
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(415) 324-0960
R SEQ ID NO: 23:
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ilarity 0.0%; E
Conservative C
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LENGTH: 1 amino acids
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NO
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INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
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(415) 32
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                             Sequence 23, Applicat
Patent No. 5587454
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                       USA
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TELEFAX: (4:
INFORMATION FOR (
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                  US-08-049-794-23
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APPLICANT: Barr, Kathryn A.
APPLICANT: Brierley, Russell A.
APPLICANT: Thill, Gregory P.
APPLICANT: Tschopp, Juerg F.
TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN
TITLE OF INVENTION: PICHIA PASTORIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                METHODS OF PRODUCING ANALGESIA AND ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1;
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400 Garden City Plaza
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                                                                                  Peter Dehlinger
We, Suite 300
                                                                                                                                                                                                                                                    Version
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0; Mismatches
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PR: 5865-0009.30
                                                                                                                                                                                                                                                                                                                                        FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415)
                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 19930415
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,759
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19930415
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Patent No. 5707828
GENERAL INFORMATION:
APPLICANT: Sreekrishna, Kotikany
                                                                 SEE: Law Offices of Petors 350 Cambridge Avenue, Palo Alto
   I, GEORGE P
METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NaN%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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0; Conservative
APPLICANT: MILJANICH, GETITLE OF INVENTION: METHITLE OF INVENTION: ENHPOWMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices
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NO
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CORRESPONDENCE ADDRESS
ADDRESSEE: Scully, S
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11530-0299
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
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                                                                                                                                                                   94306
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ZIP: 115
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                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY
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                                                                                                                  CITY:
STATE:
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Best Local S
Matches
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STATE:
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Gaps

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TELEPHONE: (202)331-7111
TELEFAX: (202) 293-6229
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 1 amino acids
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                                                                                                           peptide
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                              acid
inear
                                                                                                                                                                                                                                                                                            RESULT 11
US-07-869-933-16
; Sequence 16, Applicatic
; Patent No. 5770396
; GENERAL INFORMATION:
; APPLICANT: KINET, C
                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE:
US-07-869-933-16
                                                                                 amino
                                                                                                             TYPE:
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CITY: Al
STATE: V.
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US-08-448-606-4
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Best Local S
Matches
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                                                                                                                                                                                                                                                                                                                                                           Length 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sejlitz, Torsten
TITLE OF INVENTION: Expression System For Producing
TITLE OF INVENTION: Apolipoprotein AI-M
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/448,606
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Pollock, Vande Sande & Pride STREET: 1990 M Street, N.W., Suite 800 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Amernick, Burton A.
REGISTRATION NUMBER: 24,852
REFERENCE/DOCKET NUMBER: 0151/00121
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              Score 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SE93/01061
FILING DATE: 09-DEC-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JMBER: US/08/448,606
25-AUG-1995
                                                                   APPLICATION NUMBER: US/08/433,037
FILING DATE: 03-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: SE 9203753-0
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                            91082
                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 91087
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08448606
Patent No. 5721114
GENERAL INFORMATION:
APPLICANT: Abrahams n, Lars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abrahams n, Lars
Holmgren, Erik
Kalder n, Christina
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Mikaelsson,
                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                            Similarity
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STATE: D.C.
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE:
US-08-433-037-12
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APPLICANT:
APPLICANT:
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APPLICANT:
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US-08-448-606-4
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ISOLATION, CHARACTERIZATION, AND USE OF
THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
IMMUNOGLOBULIN
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 Length 1;
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DB 1;
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R: 40399/154 NIHD
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Mismatches
                                                                                                                                                                                                                                                                                                                      Suite 500
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                                                                                                                                                                                                                                                                                                                                                                          ZIP: 22313-0299

ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Vour APPLICATION DATA:

APPLICATION NUMBER: US/07/869,933
   Score 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JMBER: US/07/869,933
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US-08-293-150A-24
; Sequence 24, Application US/08293150A
                                                                                                                                                                    16, Application US/07869933
5. 5770396
                 Pred
                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40:
TELECOMMUNICATION INFORMATION:
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illarity 0.0%; Conservative
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(703)683-4109
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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STATE:
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Matches
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                                                           , Masahiro
POLYPEPTIDE, DNA FRAGMENT ENCODING THE
SAME AND PROCESS FOR PRODUCING THE SAME,
INHIBITION PROCESS, DRUG COMPOSITION AND
TREATING USING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                     COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/293,150A

FILING DATE: 19-AUG-1994
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Patent No. 5792629;
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: MOBUHARA, Masahiro
TITLE OF INVENTION: SAME AND PROCESS FOR PRODU
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
                                                                                                                                   STREET: P.O. BOX 1404
CITY: Alexandria
STATE: Viroi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELECOMMUNICATION INFORMATION:
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                                                  Toshinori
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(703) 836-2021
R SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 0.0%;
Matches 0; Conservative
                                                                                                                                                                                                                           Virginia
United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
                                              APPLICANT: KANAMORI, TOE
APPLICANT: NOBUHARA, MAE
TITLE OF INVENTION: POLY
TITLE OF INVENTION: SAME
TITLE OF INVENTION: INHI
TITLE OF INVENTION: TREA
NUMBER OF SEQUENCES: 110
o. 5792629
INFORMATION:
CANT: MORISHITA, F
                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
-08-293-150A-24
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US-08-293-150A-40
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   Patent No. 579
GENERAL INFOR
APPLICANT:
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GENERAL INFORMATION:
APPLICANT: Amstutz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohil, Kishorchandra
APPLICANT: Adriaenssens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Versi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION.
                                                                                                                                                                               FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   029650-049
                                                                                                                                                       MBER: US/08/293,150A
19-AUG-1994
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Sequence 23, Application US/08496847
Patent No. 5795864
                                                                                                                                                                                                                                                                                                                                                NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                    HONE: (703) 836-6620
AX: (703) 836-2021
ON FOR SEQ ID NO: 40:
E CHARACTERISTICS:
H: 1 amino acids
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ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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US-08-496-847-25

Sequence 25, Application US/08496847

Patent No. 5795864

GENERAL INFORMATION:

APPLICANT: Ametutz, Gary A.

APPLICANT: Bowersox, Stephen S.

APPLICANT: Adriaensens, Peter I.

APPLICANT: Adriaensens, Peter I.

APPLICANT: Kristipati, Ramasharma

TITLE OF INVENTION: METHODS AND

TITLE OF INVENTION: FORMULATIONS, FOR PREVENTING PROGRESSION OF NEU

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: 350 Cambridge Avenue, Suite 250

CITY: Palo Alto

STATE: CA
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.31
TELECOMMUNICATION INFORMATION:
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
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RR: 5865-0009.31
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Pred. No.
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REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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Conservative 0
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ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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TYPE: amino acid
TOPOLOGY: linear
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TOPOLOGY: linear
MECULE TYPE: protein
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HYPOTHETICAL: NO
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# ALIGNMENTS

, OTHER INFORMATION: Xaa is any residue except Asn, Cys, Gly, His, Leu, ; OTHER INFORMATION: Met, Phe or Trp	., His, M r, Ala o r, Gly, P	on US/09778885 20039748A1 Darrell C. Donald C. en KUNITZ DOMAIN POLYPEPTIDE AND METHODS FOR MAKING IT 2 NUMBER: US/09/778,885 2001-02-06 MBER: US/09/778,885 999-05-26 MBER: US/0977032 998-05-28 I Sequence polypeptide motif  Xaa is any residue except Pro, Trp or Val Xaa is leu, Glu, Met, Gln, Xaa is any residue except Tyr or Val Xaa is any residue except
	Asp, Lys, Ser,	or Met
	Asp, Lys, Ser,	facilities (ST. ST. ST. Pry
or Met		Xaa is Ard. Glu. Asn. Ala,
Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, or Met		
6) : Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, : or Met		: Ser, Thr or
Ser, Thr or Trp  Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, or Met	Cys, Gln, Gly,	: Xaa is any residue except
Xaa is any residue except Asn, Cys, Gln, Gly, P Ser, Thr or Trp Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, or Met		NAME/KEY: VAKIANT
Xaa is any residue except Asn, Cys, Gln, Gly, P Ser, Thr or Trp Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, or Met		INFORMATION: Tyr or
INFORMATION: Tyr or Val  (EY: VARIANT  FON: (5)(5)  INFORMATION: Ser, Thr or Trp  INFORMATION: Ser, Thr or Trp  KEY: VARIANT  ION: (6)(6)  INFORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, INFORMATION: or Met  KEY: VARIANT  INFORMATION: Or Met  KEY: VARIANT  ION: (7)(7)	Cys, Met, Pne,	INFORMATION: Xaa is any residue except
INFORMATION: Xaa is any residue except Arg, Cys, Met, Fne, InFORMATION: Tyr or Val  GY: VARIANT  GON: (5)(5)  INFORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, P  INFORMATION: Ser, Thr or Trp  GEY: VARIANT  ION: (6)(6)  INFORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, INFORMATION: or Met  KEY: VARIANT  INFORMATION: Or Met  KEY: VARIANT  ION: (7)(7)	4	ION: (4) (4)
ION: (4)(4) INFORMATION: Xaa is any residue except Arg, Cys, Met, Phe, T INFORMATION: Tyr or Val  GEY: VARIANT GON: (5)(5) INFORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, P INFORMATION: Ser, Thr or Trp  KEY: VARIANT GON: (6)(6) INFORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, INFORMATION: or Met  KEY: VARIANT INFORMATION: Or Met  KEY: VARIANT		NAME/KEY: VARIANT
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INFORMATION: Xaa is Leu, Glu, Met, Gln, Phe, Ser, Thr, Ala or GEY: VARIANT INFORMATION: Xaa is any residue except Arg, Cys, Met, Phe, Trp INFORMATION: Tyr or Val GEY: VARIANT INFORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, Phe INFORMATION: Ser, Thr or Trp GEY: VARIANT INFORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, Ty INFORMATION: Cor Met KEY: VARIANT INFORMATION: Or Met KEY: VARIANT INFORMATION: Or Met KEY: VARIANT		INDIATION: (3)
INFORMATION: Xaa is Leu, Glu, Met, Gln, Phe, Ser, Thr, Ala or INFORMATION: Xaa is Leu, Glu, Met, Gln, Phe, Ser, Thr, Ala or Gon: (4)(4) INFORMATION: Xaa is any residue except Arg, Cys, Met, Phe, Trp INFORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, Phe INFORMATION: Ser, Thr or Trp Con: (5)(5) INFORMATION: Ser, Thr or Trp Con: (6)(6) INFORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, Ty INFORMATION: or Met KEY: VARIANT INFORMATION: Or Met KEY: VARIANT INFORMATION: Or Met KEY: VARIANT		INFORMATION: FIG, 11P OF
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INFORMATION: Xaa is any residue except Asp, Cys, Ciy, Air, Thrormation: Pro, Trp or Val  GEY: VARIANT  ION: (3)(3)  INFORMATION: Xaa is Leu, Glu, Met, Gln, Phe, Ser, Thr, Ala or  GEY: VARIANT  ION: (4)(4)  INFORMATION: Xaa is any residue except Arg, Cys, Met, Phe, Trp  INFORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, Phe  INFORMATION: Ser, Thr or Trp  GEY: VARIANT  ION: (5)(5)  INFORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, Ty  INFORMATION: Or Met  KEY: VARIANT  ION: (7)(7)	יינט טייט	$(2)\ldots(2)$
INFORMATION: Xaa is any residue except Asp, Cys, Gly, His, Met INFORMATION: Pro, Trp or Val GY: VARIANT INFORMATION: Xaa is Leu, Glu, Met, Gln, Phe, Ser, Thr, Ala or INFORMATION: Xaa is any residue except Arg, Cys, Met, Phe, Trp INFORMATION: Tyr or Val GY: VARIANT GY: VARIANT GY: VARIANT TON: (5)(5) INFORMATION: Ser, Thr or Trp INFORMATION: Ser, Thr or Trp GYS, VARIANT GYS, VARIANT INFORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, Ty INFORMATION: Commet GY: VARIANT GYS, CAN, GAN, Ala, Val, Asp, Lys, Ser, Ty INFORMATION: Or Met KEY: VARIANT INFORMATION: Or Met KEY: VARIANT INFORMATION: Or Met KEY: VARIANT ION: (7)(7)		VARIANT
CEY: VARIANT  CON: (2)(2)  INFORMATION: Xaa is any residue except Asp, Cys, Gly, His, Met INFORMATION: Pro, Trp or Val  CEY: VARIANT  CON: (3)(3)  INFORMATION: Xaa is Leu, Glu, Met, Gln, Phe, Ser, Thr, Ala or Gry: VARIANT  INFORMATION: Tyr or Val  CEY: VARIANT  CON: (5)(5)  INFORMATION: Ser, Thr or Trp  CEY: VARIANT  CON: (6)(6)  INFORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, Ty INFORMATION: Or Met  CEY: VARIANT  CON: (6)(6)  INFORMATION: Or Met  CEY: VARIANT  CON: (7)(7)		polypeptide
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ING DATE: 1999-05-26 JICATION NUMBER: US 60/087,032 SEQ ID. NOS: 20 FastSEQ for Windows Version 3.0 FastSEQ for Windows Version 3.0  Artificial Sequence SEMATION: polypeptide motif Artificial Sequence SORMATION: Xaa is any residue except Asp, Cys, Gly, His, Met SORMATION: Xaa is any residue except Arg, Cys, Gly, His, Met SORMATION: Xaa is any residue except Arg, Cys, Met, Phe, Trp FORMATION: Xaa is any residue except Arg, Cys, Gln, Gly, Phe FORMATION: Xaa is any residue except Ash, Cys, Gln, Gly, Phe FORMATION: Xaa is any residue except Ash, Cys, Gln, Gly, Phe FORMATION: Ser, Thr or Trp SORMATION: Ser, Thr or Trp		Ą
LICATION NUMBER: 09/320,095 LICATION NUMBER: 1990-05-26 LICATION NUMBER: US 60/087,032 LICATION NUMBER: US 60/087,032 LICATION NUMBER: US 60/087,032 LICATION NUMBER: US 60/087,032 SEQ ID.NOS: 20 SEC ID		
LING DATE: 2001-02-06 LICATION NUMBER: 09/320,095 LICATION NUMBER: 09/320,095 LICATION NUMBER: 09/320,095 LICATION NUMBER: US 60/087,032 LICATION NUMBER: US 60/087,032 SEQ ID.NOS: 20 FastSEQ for Windows Version 3.0 FastSEQ for Windows Version 3.0 LATLificial Sequence CORMATION: Dolypeptide motif LATLificial Sequence CORMATION: Xaa is any residue except Asp, Cys, Gly, His, Met CORMATION: Xaa is leu, Glu, Met, Gln, Phe, Ser, Thr, Ala or CORMATION: Xaa is any residue except Arg, Cys, Met, Phe, Trp CORMATION: Tyr or Val CAL: (4)(4) CORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, Phe CORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, Phe CORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, Ty CORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, Ty CORMATION: CALL CALL CALL CALL CALL CALL CALL CAL		A L
MACHICATION NUMBER: US/09/778,885 LING DATE: 2001-02-06 LICATION NUMBER: 09/320,095 LICATION NUMBER: 09/320,095 LICATION NUMBER: 09/320,095 LICATION NUMBER: 05-26 LICATION NOS: 20 LICATION N		AND MEIRODS FOR FEMALING
TWO MAILON:  THE NOTE:  THE NOTE:	STUTENT	KUNITZ DOMAIN POLIFEFIIDE AND METHODS BOD MAKING IT
NYBERTION: NOBLICAL DOMAIN POLITERING IT  EBNCE: 98-22  EBNCE: 98-22  LING DATE: 2001-02-06  LICATION NUMBER: US 60/087,032  NG DATE: 1999-05-26  LICATION NUMBER: US 60/087,032  NG DATE: 1998-05-28  SEQ ID NOS: 20  SEQ ID	MATERIALS.	en mariana postata por vogenaton
Gao, Zeren Garrion Garri		Donald
FOSTER, DORALD C.  Gao, Zeren  Gao, Zeren  Gao, Zeren  Gao, Zeren  Gao, Zeren  KUNITZ DOMAIN POLYPEPTIDE AND MATERIALS  INVENTION: AND METHODS FOR MAKING IT  ENCE: 98-22  LILING DATE: 1999-05-26  LICATION NUMBER: 05/087,032  ING DATE: 1999-05-28  ING DATE: 1999-05-28  SEQ ID NOS: 20  FASTERO FOR Windows Version 3.0  FASTERO FOR Windows Version 3.0  FARTIFICIAL Sequence  ORMATION: Xaa is any residue except Asp, Cys, Gly, His, Met ORMATION: Xaa is Leu, Glu, Met, Gln, Phe, Ser, Thr, Ala or VARIANT  (3)(3)  (3)(3)  CORMATION: Xaa is any residue except Arg, Cys, Met, Phe, Trp CORMATION: Xaa is any residue except Arg, Cys, Met, Phe, Trp CORMATION: Xaa is any residue except Arg, Cys, Met, Phe, Trp CORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, Phe CORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, Phe CORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, Phe CORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, Phe CORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, Phe CORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, Ty CORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, Ty CORMATION: Cor Met  (5)(6)  FORMATION: Cor Met  (7)(7)  (7)(7)  (7)(7)  (7)(7)  (7)(7)		Darrell
CONALID. Darrell C. Gao. Zeren Ga		•
Conklin.  Conkli		Publication No. US20020039748A1
NO. USSO20039748A1 ORMATION: CONKAILON. CONKAILON CON		uence 5, Application
Sequence 5, Application US/09778885  Publication No. US2020039748A1  GENERAL INFORMATION:  APPLICANT: CONKIIN, Darrell C.  APPLICANT: CONKIIN, Darrell C.  APPLICANT: CONKIIN, Darrell C.  APPLICANT: GOALINO, WUNTER DOMAIN POLYBEPTIDE AND MATERIALS  TITLE OF INVENTION: AND METHODS FOR MAKING IT  TITLE OF INVENTION: WUNBER: US/09/778,885  CURRENT APPLICATION NUMBER: US/09/778,885  CURRENT FILING DATE: 198-05-28  RIOR FILING DATE: 198-06-28  NUMBER OF SEQ ID NOS: 20  SOFTWARE: FASTSEQ for WINGOWS Version 3.0  SOFTWARE: FASTSEQ for WINGOWS Version 3.0  SEQ ID NO 5  LENGTH: 51  TYPE: PRT  ORGANISM: Artificial Sequence  FRAUTHS: INFORMATION: PRO, TTP Or Val  NAME/KEY: VARIANT  LOCATION: (2): (2): (2)  OTHER INFORMATION: Pro, TTP Or Val  NAME/KEY: VARIANT  LOCATION: (3): (3): (4)  OTHER INFORMATION: Yaa is any residue except AFG, Cys, Gln, Gly, Phe  OTHER INFORMATION: Yaa is any residue except AFG, Cys, Gln, Gly, Phe  OTHER INFORMATION: Yar or Val  NAME/KEY: VARIANT  LOCATION: (4): (4)  OTHER INFORMATION: Xaa is any residue except AFG, Cys, Gln, Gly, Phe  OTHER INFORMATION: Xaa is any residue except AFG, Cys, Gln, Gly, Phe  OTHER INFORMATION: Xaa is any residue except AFG, Cys, Gln, Gly, Phe  OTHER INFORMATION: Xaa is any residue except AFG, Cys, Gln, Gly, Phe  OTHER INFORMATION: Xaa is any residue except AFG, Cys, Gln, Gly, Phe  OTHER INFORMATION: Xaa is any residue except AFG, Cys, Gln, Gly, NAME/KEY: VARIANT  LOCATION: (5):(5)  OTHER INFORMATION: Or Met  NAME/KEY: VARIANT  LOCATION: (5):(6)  OTHER INFORMATION: Or Met  NAME/KEY: VARIANT  LOCATION: (7):(7)  OTHER INFORMATION: OR Met		-09-778-885-5

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APPLICANT: Bergmann, John
TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated
FILE REFERENCE: 3033.1003-001
CURRENT APPLICATION NUMBER: US/09/909,348
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/219,800
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 14
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Patent No. US20020137119A1
GENERAL INFORMATION:
APPLICANT: Emil Israel Katz
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF
TITLE OF INVENTION: UTILIZING EACH
TITLE OF INVENTION: UTILIZING EACH
FILE REFERENCE: 01/2283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: Patentin version 3.1
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Pred. No. 0;
0; Mismatches
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OTHER INFORMATION: Xaa at position six is GlOTHER INFORMATION: Xaa at position thirteen
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Mismatches
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TITLE OF INVENTION: PEPTIDES REPRESENTATIVE
TITLE OF INVENTION: DIRECTED THEREAGAINST,
TITLE OF INVENTION: UTILIZING EACH
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CURRENT APPLICATION NUMBER: US/09/982,172
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Patent No. US20020137119A1
GENERAL INFORMATION:
                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
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ilarity 0.0%;
Conservative
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ilarity 0.0%;
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Best Local Similarity
Matches 0; Conser
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US-09-982-172-3
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Best Local S
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                                                                                                                                                                                                                                                                                            Gly,
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OTHER INFORMATION: Xaa is any residue except Asn, Asp, Cys, His,
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                                                    Asp,
                                                                                                                                                               Phe,
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INFORMATION: Xaa is Ala, Lys, Ser, Leu, Thr, Ile,
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OTHER INFORMATION: Xaa is any residue except Ala, Asp, OTHER INFORMATION: Met, Trp or Tyr
NAME/KEY: VARIANT
LOCATION: (16)...(16)
OTHER INFORMATION: Xaa is Ser, Ala, Arg, Val, Gln, Lys, NAME/KEY: VARIANT
LOCATION: (17)...(17)
OTHER INFORMATION: Xaa is Phe, Tyr, Ile, Trp or Leu
                                                                                                                                                                                                                                                                            LOCATION: (14)...(14)
OTHER INFORMATION: Xaa is any residue except Arg, Asn,
OTHER INFORMATION: Ser, Trp or Tyr
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                                                                                                                                                                                                                               Cys,
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OTHER INFORMATION: Xaa is any residue except Cys, Met,
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LOCATION: (13)...(13)
OTHER INFORMATION: Xaa is any residue except Asp,
OTHER INFORMATION: Or Trp
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                                                                                                 residue except Ala,
d Val
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OTHER INFORMATION: Xaa is Tyr, His, Phe, Trp,
                                                                                                                                                                  Asp,
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LOCATION: (24)...(24)
OTHER INFORMATION: Xaa is Lys, Gln, Asn, His,
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                                                    is Pro, Arg, Leu, Val,
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OTHER INFORMATION: Xaa is Arg, Lys, Ala,
OTHER INFORMATION: and Ser
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LOCATION: (20)...(20)
OTHER INFORMATION: Xaa is Lys, Asn, Ser
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Sequence 4, Application US/09909348
Patent No. US20020042373A1
GENERAL INFORMATION:
APPLICANT: Carney, Darrell H.
APPLICANT: Crowther, Roger S.
                                                                                                                Trp and
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LOCATION: (21)...(21)
OTHER INFORMATION: Xaa is any
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LOCATION: (19)...(19)
OTHER INFORMATION: Xaa is Tyr
                                                                                 LOCATION: (11)...(11)
OTHER INFORMATION: Xaa is any
OTHER INFORMATION: Pro, Trp ar
    is Gly
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0.0%;
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Crowther, Roger S
Stiernberg, Janet
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                 NAME/KEY: VARIANT
LOCATION: (9)...(9)
OTHER INFORMATION: Xaa
    INFORMATION: Xaa
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LOCATION: (23)
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US-09-9
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GENERAL INFORMATION:
APPLICANT: Emil Israel Katz
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND MI
TITLE OF INVENTION: UTILIZING EACH
FILE REFERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: Patentin version 3.1
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US-09-982-172-19
; Sequence 19, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF
; TITLE OF INVENTION: UTILIZING EACH
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Score 0; DB 3
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TITLE OF INVENTION: UTILIZING EACH
FILE REFERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
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US-09-982-172-31.
; Sequence 31, Application US/09982172
; Patent No. US20020137119A1
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ORGANISM: Artificial sequence
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GENERAL INFORMATION:
APPLICANT: Emil Israel Katz
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF
TITLE OF INVENTION: DIRECTED THEREAGAINST, ANI
TITLE OF INVENTION: UTILIZING EACH
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TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF; TITLE OF INVENTION: UTILIZING EACH; FILE REFERENCE: 01/22283.
CURRENT APPLICATION NUMBER: US/09/982,172; CURRENT FILING DATE: 2001-10-19; NUMBER OF SEQ ID NOS: 253; SOFTWARE: PatentIn version 3.1
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CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: Patentin version 3.1
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Patent No. US20020137119A1
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      CURRENT FILING DATE: 2001-10-
NUMBER OF SEQ ID NOS: 253
SOFTWARE: Patentin version 3.1
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ORGANISM: Artificial sequence
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ORGANISM: Artificial
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     SOFTWARE: Patentin version
SEQ ID NO 46
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TYPE: PRT
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Matches 0; Conser
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Best Local Similarity
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; OTHER INFORMATION:
US-09-982-172-46
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Sequence 37, Application US/09982172
Sequence 37, Application US/09982172
Sequence 37, Application US/09982172
Sequence 37, Application US/09982172
Sequence 37, Application:
Patent No. US20020137119A1
GENERAL INFORMATION:
APPLICANT: Emil Israel Katz
TITLE OF INVENTION:
TITLE OF INVENTION:
UTILIZING EACH
TITLE OF INVENTION:
UTILIZING EACH
FILE REFERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: Patentin version 3.1
SEQ ID NO 37
LENGTH: 1
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TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIE
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAL
TITLE OF INVENTION: UTILIZING EACH
FILE REFERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
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Sequence 35, Application US/09982172;
Patent No. US20020137119A1
GENERAL INFORMATION:
APPLICANT: Emil Israel Katz
TITLE OF INVENTION: DIRECTED THEREAGAINST, ANI
TITLE OF INVENTION: UTILIZING EACH
FILE REFERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: Patentin version 3.1
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; Patent No. US20020137119A1
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APPLICANT: Emil Israel Katz
TITLE OF INVENTION: DIRECTED THEREAGAINST, ANI
TITLE OF INVENTION: UTILIZING EACH
FILE REFERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172; CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: PatentIn version 3.1
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; APPLICANT: Emil Israel Katz; TITLE OF INVENTION: DIRECTED THEREAGAINST, ANITITLE OF INVENTION: UTILIZING EACH; TITLE OF INVENTION: UTILIZING EACH; FILE REFERENCE: 01/22283; CURRENT APPLICATION NUMBER: US/09/982,172; CURRENT FILING DATE: 2001-10-19; NUMBER OF SEQ ID NOS: 253; SOFTWARE: Patentin version 3.1; SEQ ID NO 69; LENGTH: 1
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RESULT 15
US-09-982-172-83
is Sequence 83, Application US/09982172
is Sequence 83, Application US/09982172
is Patent No. US20020137119A1
is GENERAL INFORMATION:
it APPLICANT: Emil Israel Katz
it TILE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAL
it TILE OF INVENTION: UTILIZING EACH
it TILE OF INVENTION: UTILIZING EACH
it FILE REFERENCE: 01/22283
it CURRENT APPLICATION NUMBER: US/09/982,172
it CURRENT FILING DATE: 2001-10-19
it NUMBER OF SEQ ID NOS: 253
it CORRENT PLAND METHON OF SEQ ID NOS: 253
it CORRENT PLAND METHON OF SEQ ID NOS: 253
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US-09-982-172-81
; Sequence 81, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil 1srael Katz
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND TITLE OF INVENTION: UTILIZING EACH
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
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; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-83
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Pred. No. 0;
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Similarity 0.0%;
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RESULT 2
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; Sequence 1142, Application US/11050857
; Publication No. US20060040278A1
; GENERAL INFORMATION:
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US-11-264-096-186

US-11-264-096-186

US-11-264-096-119

US-11-264-096-1045

US-11-264-096-1045

US-11-264-096-1119

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US-11-148-262-1

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US-11-148-262-9

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US-11-078-256-279

Sequence 279, Application US/11078256

Publication No. US20060035814A1

GENERAL INFORMATION:

APPLICANT: Brophy, Colleen

APPLICANT: Romalavilas, Padmini

APPLICANT: Panitch, Alyssa

APPLICANT: Seal, Lokesh

APPLICANT: Seal, Brandon L.

TITLE OF INVENTION: REAGENTS AND METHODS FOR SMO

FILE REFERENCE: 03-223-US

CURRENT APPLICATION NUMBER: US/11/078,256

CURRENT APPLICATION NUMBER: 60/314,535

PRIOR APPLICATION NUMBER: 60/314,535

PRIOR APPLICATION NUMBER: 60/314,535

PRIOR APPLICATION NUMBER: Sols-03-11

PRIOR APPLICATION NUMBER: Patentin version 3.1

SOFTWARE: Patentin version 3.1

SEQ ID NO 279
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ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic |
FEATURE:
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LOCATION: (1)...(1)
OTHER INFORMATION: X is
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US-11-144-947-611
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APPLICANT: Compugen Ltd
TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES,
TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 1847.1005
CURRENT APPLICATION NUMBER: US/11/050,857
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 1150
SEQ 'ID NO 1142
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TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2C2
CURRENT APPLICATION NUMBER: US/11/144,947
CURRENT FILING DATE: 2005-06-06
PRIOR APPLICATION NUMBER: 09/882,171
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Pred. No. 0;
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R FILING DATE: 2001-03-16

R FILING DATE: 2001-03-16

R APPLICATION NUMBER: 60/190,068

R FILING DATE: 2000-03-17

R APPLICATION NUMBER: 10/164,861

R FILING DATE: 2002-06-10

R APPLICATION NUMBER: 09/149,476

R APPLICATION NUMBER: 09/149,476

R APPLICATION NUMBER: 60/040,162

R APPLICATION NUMBER: 60/040,162

R APPLICATION NUMBER: 60/040,162

R APPLICATION NUMBER: 60/040,333

R FILING DATE: 1997-03-07
                                                                                                                                                                 ; OTHER INFORMATION: Synthetic peptide US-11-050-857-1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/040,333
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/038,621
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APPLICATION NUMBER: 60/040,626
FILING DATE: 1997-03-07
ning Prior Application data rem
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Sequence 395, Application US/11144947
Publication No. US20060084082A1
GENERAL INFORMATION:
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WARE: Patentin Ver.
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                                                                       TITLE OF INVENTION: 186 Human Secreted proteins;
FILE REFERENCE: PZ002P2C2
CURRENT APPLICATION NUMBER: US/11/144,947
CURRENT FILING DATE: 2005-06-06
PRIOR APPLICATION NUMBER: 09/882,171
PRIOR FILING DATE: 2005-06-03
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2000-03-17
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publication No. US20060084794A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Albumin Fusion Proteins

FILE REFERENCE: PF546D1

CURRENT APPLICATION NUMBER: US/11/264,096

CURRENT FILING DATE: 2005-11-02

PRIOR FILING DATE: 2001-04-12

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-12-21

PRIOR FILING DATE: 2000-04-25
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Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 761
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FILING DATE: 1997-03-07
Application US/11144947
. US20060084082A1
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FILING DATE: 2002-06-10
APPLICATION NUMBER: 09/
                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1998-09-08
APPLICATION NUMBER: PCT
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US-11-264-096-184
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; Sequence 744, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
                                                                                                                                                                           APPLICANT: Rosen et al.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546D1
CURRENT APPLICATION NUMBER: US/11/264,096
CURRENT FILING DATE: 2005-11-02
PRIOR APPLICATION NUMBER: 09/833,245
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-12-21
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o. US20060084794A1
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SOFTWARE: PatentIn V
                                                                                                                              Sequence 500, Applic
Publication No. US20
GENERAL INFORMATION:
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US-11-264-096-744
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 DB 11;
                                                                                                                                                                               Sequence 186, Application US/11264096

Publication No. US20060084794A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Albumin Fusion Proteins

FILE REFERENCE: PF546D1

CURRENT APPLICATION NUMBER: US/11/264,096

CURRENT FILING DATE: 2005-11-02

PRIOR APPLICATION NUMBER: 09/833,245

PRIOR FILING DATE: 2001-04-12

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-12-21

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 2267

SOFTWARE: PATENTIN Ver. 2.1
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FILE REFERENCE: PF546D1
CURRENT APPLICATION NUMBER: US/11/264,096
CURRENT FILING DATE: 2005-11-02
PRIOR APPLICATION NUMBER: 09/833,245
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 325
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Publication No. US20060084794A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
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ilarity 0.0%; 1
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US-11-264-096-186
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US-11-264-096-186
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APPLICANT: CanBas Co., Ltd.
APPLICANT: Kawabe, Takumi
APPLICANT: Kawabe, Takumi
APPLICANT: Kawabe, Takumi
APPLICANT: Kobayashi, Hidetaka
TITLE OF INVENTION: PEPTIDES AND PEPTIDOMIMETICS HAVING IMMUNE-MODULATING, ANTI-
TITLE OF INVENTION: INFLAMMATORY, AND ANTI-VIRAL ACTIVITY
FILE REFERENCE: 087533-0309084
CURRENT APPLICATION NUMBER: US/10/877,961B
CURRENT FILING DATE: 2004-06-25
PRIOR FILING DATE: 2004-06-25
PRIOR FILING DATE: 2003-06-25
PRIOR FILING DATE: 2003-06-25
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Mismatches
RESULT 12
US-11-264-096-1546

Sequence 1546, Application US/11264096

Publication No. US20060084794A1

GENERAL INFORMATION:

TITLE OF INVENTION: Albumin Fusion Proteins

FILE REFERENCE: PF546D1

CURRENT FILING DATE: 2005-11-02

PRIOR APPLICATION NUMBER: 09/833,245

PRIOR APPLICATION NUMBER: 60/229, 358

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-12-21

SOFTWARE: Patentin Ver. 2.1

SEQ ID NOS: 2267
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OS: 255
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Sequence 121, Application US/10877961B
Publication No. US20060003941A1
GENERAL INFORMATION:
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ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Description
FEATURE:
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OTHER INFORMATION: Positions 1
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ilarity 0.0%;
Conservative
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PRIOR APPLICATION NUMBER: 60,
PRIOR FILING DATE: 2003-06-2
NUMBER OF SEQ ID NOS: 255
SOFTWARE: PatentIn version 3
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0-877-961B-121
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LOCATION: (1).
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TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546D1
CURRENT APPLICATION NUMBER: US/11/264,096
CURRENT FILING DATE: 2005-11-02
                                                                                                                                                APPLICANT: Rosen et al.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PFS46D1
CURRENT APPLICATION NUMBER: US/11/264,096
CURRENT FILING DATE: 2005-11-02
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PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
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PRIOR FILING DATE: 2001-04-12
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PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1119
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                                                                                            Sequence 1045, Application US/11264096
Publication No. US20060084794A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
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US-11-264-096-1045
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US-10-913-711B-22
; Sequence 22, Application US/10913711B
; Publication No. US20060014157A1
; GENERAL INFORMATION:
; APPLICANT: CanBas Co., Ltd.
; APPLICANT: Kawabe, Takumi
; APPLICANT: Kobayashi, Hidetaka
; TITLE OF INVENTION: SENSITIVITY TEST TO PREDICT EFFICACY OF ANTI-CANC
; FILE REFERENCE: 087533-0310448
; CURRENT APPLICATION NUMBER: 60/494,022
; PRIOR APPLICATION NUMBER: 60/494,022
; PRIOR FILING DATE: 2003-08-06
; NUMBER OF SEQ ID`NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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US-10-509-095A-40
; Sequence 40, Application US/10509095A
; Publication No. US20060036073A1
; GENERAL INFORMATION:
; APPLICANT: WINDISCH, MANFRED
; TITLE OF INVENTION: NEUROTROPHIC AND NEUROPROTECTIVE PEPTIDES
; FILE REFERENCE: 4301-1117
; CURRENT APPLICATION NUMBER: US/10/509,095A
; CURRENT FILING DATE: 2004-09-28
; PRIOR PILING DATE: 2003-03-28
; PRIOR FILING DATE: 2003-03-28
; PRIOR FILING DATE: 2002-03-28
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: Description of Artificial Sequence:
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Pred. No. 0;
0; Mismatches
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; OTHER INFORMATION: Xaa is D-Cyclohexyl-alanine
US-10-913-711B-22
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LOCATION: (1)..(2)
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OTHER INFORMATION: Xaa is
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SOFTWARE: Patentin Ver.
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LENGTH: 2
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TYPE: PRT
ORGANISM: Artificial Sequence
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COTHER INFORMATION: Description of Artificial Sequence: Synthetic
COTHER INFORMATION: peptide
US-10-509-095A-40

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Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps
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-252-991A-	52-991A-3136	-209-5	2-991A-25	-303-5	7	-630-915A-	-879-957-3	-142-231-8	-627-650B-	-09-436-	-627-650B-	-436-063C-	-627-650B-	36-063C-	-09-627-650B-	US-09-436-063C-9	6-436-3
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RESULT 1
US-08-727-688-23
Sequence 23, Application US/08727688
Sequence 23, Application US/08727688
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road D377/AP6D
CITY: Abbott Park
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0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla E
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 596
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TELEPHONE: (847) 937-0378
TELEFAX: (847) 938-2623
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COMPUTER READABLE FORM:
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SOFTWARE: FABESEO
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TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR
TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC
TITLE OF INVENTION: TARGET PROTEINS
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; Sequence 44409, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and protei;
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                        Score 18;
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,999
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31307
LENGTH: 438
                           1999-02-18
ER: US 60/074,788
                                                                            60/094,190
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Pred. N
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Patent No. 5434064
GENERAL INFORMATION:
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Skolnik, Edward Y.
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CORRESPONDENCE ADDRESS
ADDRESSEE: Browdy at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: (SOFTWARE: Patentin Ver EQ ID NO 44409 LENGTH: 777
                                                                                                                                                                            Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Drosophila
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; ORGANISM: Pseudo
US-09-252-991A-31307
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APPLICANT:
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US-07-906-34; Sequence
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25365
LENGTH: 191
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATI
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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pred. No. 0.36;
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US-09-252-991A-31307
; Sequence 31307, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                        NO.
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US-09-252-991A-25365
; Sequence 25365, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
                                                                                  Sequence 17897, Application US/09252991A
Patent No. 6551795
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US-09-252-991A-25365
                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17897
LENGTH: 167
                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa
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APPLICANT: Marc J.
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                    Patent No. 6551795
GENERAL INFORMATION:
                                                     RESULT 2
US-09-252-991A-17897
                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudo - 09-252-991A-17897
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Human Protease and Use of Such Protease for Pharmaceutical Applications and for Reducing the Allergenicity of No. 6642011 Proteins
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Sequence 2, App...
General No. 6642011
General INFORMATION:
TITLE OF INVENTION: Human Protease and Use of TITLE OF INVENTION: Applications and for Redurithe OF INVENTION: Proteins
TITLE OF INVENTION: Proteins
FILE REFERENCE: GC532
CURRENT APPLICATION NUMBER: US/09/060,8548
CURRENT FILING DATE: 1998-04-15

MITMBER OF SEQ ID NOS: 7
FARESCE FOR WINDOWS Version 3.0
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TITLE OF INVENTION: Bleaching compositions
TITLE OF INVENTION: protease variants
FILE REFERENCE: Bleaching comp comprising m
CURRENT APPLICATION NUMBER: US/09/529,904
CURRENT FILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: PCT/AU98/00562
PRIOR FILING DATE: 1998-07-17
PRIOR APPLICATION NUMBER: PO 8088
PRIOR FILING DATE: 1997-07-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
                                                                                                                                                                                                      Score 18;
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Patent No. 6831053
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Naki, Donald P.
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Baeck, Andre C.
Ohtani, Ryohei (nmn)
Busch, Alfred (nmn)
Showell, Michael S.
Poulose, Ayrookaran J
Schellenberger, Volke
Kellis, Jr., James T.
Paech, Christian (nmn)
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SEQ ID NO 2
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US-09-529-904-3
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Sequence 6, Application US/09463048A
Patent No. 6630619
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Research Organi
APPLICANT: EAST, Peter David
TITLE OF INVENTION: Toxin Genes from the Bacteria Xenorhabdus nen
TITLE OF INVENTION: luminescens
FILE REFERENCE: 050179-0076
CURRENT APPLICATION NUMBER: US/09/463,048A
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      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Neisserial Antigens
FILE REFERENCE: CHIR0160
CURRENT APPLICATION NUMBER: US/09/303,518D
CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 1098
SOFTWARE: PatentIn version 3:1
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Mismatches
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                                                               APPLICATION NUMBER: US/07/906,349A
FILING DATE: 30-JUN-1992
CLASSIFICATION: 435
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Pred. N
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US-09-303-518D-195
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                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 20.0%;
2; Conservative (
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                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/6
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
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TOPOLOGY: lir
MOLECULE TYPE:
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US-09-463-048A-6
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SNGTH: 1152
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SEE: Pioneer Hi-Bred International, Inc: 700 Capital Square, 400 Locust Street
Des Moines
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High Threonine Derivatives
Alpha-Hordothionin
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Scarlato, Vincenzo
APPLICANT: Masignani, Vega
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Neisserial Antigens
FILE REFERENCE: CHIR0160
CURRENT APPLICATION NUMBER: US/09/303,518D
CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 1098
SOFTWARE: PatentIn version 3.1
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
                                                                                                                                                                                                                                                                              Sequence 879, Application US/09303518D Patent No. 6914131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/459,180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08824379 Satent No. 5885801 GENERAL INFORMATION: APPLICANT: Rao, A. Gururai
                                          ; ORGANISM: Caenorhabditis elegans
US-09-436-063C-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis
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illarity 20.0%; Conservative 0
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TITLE OF INVENTION: High
TITLE OF INVENTION: Alph
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                1058
                                                                                                                                 Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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OPERATING SYSTEM:
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US-09-303-518D-879
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   SEQ ID NO 5
LENGTH: 1917
TYPE: PRT
ORGANISM: Cae
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LENGTH: 2616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S-08-824-379-3
Sequence 3, Ap
Patent No. 588
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US-09-303-
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Patent No. 6407210
GENERAL INFORMATION:
APPLICANT: Bamber, Bruce
APPLICANT: Jorgensen, Erik
TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptor
TITLE OF INVENTION: Methods Related Thereto
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; Sequence 5, Application US/09627650B
; Patent No. 6406872
; GENERAL INFORMATION:
   APPLICANT: Bamber, Bruce
; TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Rec; TITLE OF INVENTION: Methods Related Thereto
; TITLE REFERENCE: 21101.0009U3
; FILE REFERENCE: 21101.0009U3
; CURRENT APPLICATION NUMBER: US/09/627,650B
; PRIOR APPLICATION NUMBER: 09/436,063
; PRIOR FILING DATE: 1999-11-08
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.1
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CURRENT APPLICATION NUMBER: US/09/436,063C
CURRENT FILING DATE: 1999-11-08
CURRENT FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 08/956,323
PRIOR FILING DATE: 1997-10-23
PRIOR APPLICATION NUMBER: US 08/956,564
PRIOR FILING DATE: 1997-10-23
PRIOR FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18;
                                                                                                                                                                                                   ; ORGANISM: Bacillus amyloliquefaciens US-09-529-904-3
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PRIOR FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
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TYPE: PRT
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Score 18; Pred: No. 0

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TITLE OF INVENTION: MODIFIED-AFFINITY STREPTAVIDIN
NUMBER OF SEQUENCES: 11
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01720
FILING DATE:
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Pred. No. 1.2;
0; Mismatches
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,055
FILING DATE: 09-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 16336-5PC
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Simon, Soma G.

REGISTRATION NUMBER: 37,444

REFERENCE/DOCKET NUMBER: 354-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 515-248-4896

TELEFAX: 515-248-4896

TELEFAX: 515-248-4896

TELEFAX: 515-248-4896

TELEFAX: 515-248-4896

TELEFAX: 155-248-4896

TELEFAX: 155-248-4896

TELEFAX: 1100 NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 45 amino acids

TYPE: amino acid

TYPE: amino acid

TYPE: 1inear
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ilarity 20.0%;
Conservative
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Matches 2; Conser
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; MOLECULE TYPE:
PCT-US96-01720-9
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
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Biocceleration Ltd
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(c) 1993
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Title: Derfact acore:	US-10-046-922-33
Sequence:	1 CXXXXXXXX 10
Scoring table:	BLOSUM62
1	Gapop 10.0 , Gapext 0.5

2443163 hits satisfying chosen parameters: 439378781 residues 2443163 segs, o£ Total number Searched:

summaries 100% 45 St Post-processing: Minimum Match 0% Maximum Match 10 Listing first 45 seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Geneseq\_21:\*
geneseqp1980s:\*
geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2002s:\*
geneseqp2003as:\*
geneseqp2003as:\* Database

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, , derived by analysis of the total score distribution. NON : score gand is Pred

	Description	247471	3053	3053	m93527 Human	31230 Human	30690 Human	1474	69151 Pseudo	12185 Human	0794 Human	30793 Human	30806	76619 Pseudo	5621	p30	31485	3047	31412 Human se	30500 Human	3132	p314	119	2528	0702 Human se
SUMMARIES	ID	DZ4	ADP30533	3053	352	ന	ADP30690 -		15	1218	3079	79	3080	ABO76619	5621	P3092	3148	ADP30479	3141	P3050	P313	DP3147	ADP31192	œ	P3070
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8 ADP31441 4 ABG21039 8 ADP31267	P3050	ADP3121	ADP31 ADP31	AB08256	ADP3085	8 ADP31227	ADP3085	ADP3141	ADP3141	. ADP316	ADZ5620	ADZ56	ADP3086	ADP30	8 ADP30941
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## ALIGNMENTS

hyaluronan synthase; HAS; hyaluronidase; HYAL; HAS1; HAS2; HAS3; HYAL1; HYAL2; HAL3; PH-20; cancer; hyperproliferation; inflammation; anabolic; hypertensive; gynaecological; neuroprotective; antianemic; cytostatic; anti-inflammatory; endocrine-gen; immunosuppressive; gene therapy. standard; peptide; 30 AA 50 2004WO-AU001383 SEQ ID NO entry) (first Alu sense peptide WO2005035548-A1. 11-OCT-2004; Unidentified 30-JUN-2005 21-APR-2005 ADZ47471; ADZ47471 RESULT 1 ADZ47471 

10-OCT-2003; 2003AU-00905551 01-DEC-2003; 2003AU-00906658 (MEDI-) MEDITECH RES LTD GR; Brownlee 2005-315540/32 ŢŢ, Brown WPI;

beta-2 Novel compound capable of reducing level, function or activity of hyaluronan synthase or hyaluronidase, useful for treating cancer, hyperproliferative condition, , A-beta-lipoproteinemia, A-V, A be microglobulin amyloidosis.

SEQ ID NO 50; 277pp; English. 22; Example

This invention describes a novel nucleic acid molecule capable of reducing the level of hyaluronan synthase (HAS) or hyaluronidase (HYAL) or the function or activity of HAS or HYAL. HAS is selected from HAS1, HAS2 and HAS3. HYAL is chosen from HYAL1, HYAL2, HAL3 and PH-20. The nucleic acid molecule is an oligonucleotide or its chemically modified form comprising a chemically modified backbone or a non-natural form comprising a chemically modified backbone or a non-natural internucleoside linkage. The compound is an interactive molecule capable of binding or otherwise associating with HAS and/or HYAL to reduce HAS

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17-SEP-2002;
17-SEP-2003;
02-MAY-2003;
02-MAY-2003;
02-MAY-2003;
02-MAY-2003;
02-MAY-2003;
02-MAY-2003;
02-MAY-2003;
02-MAY-2003;
03-JUL-2003;
08-JUL-2003;
08-JUL-2003;
14-JUL-2003;
15-JUL-2003;
08-AUG-2003;
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Halenbeck RF
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                                                                   endocrine-
ts a peptide
n describes
and/or HYAL function or activity. The novel molecule is useful for treating cancer, hyperproliferative conditions or inflammatory conditions. The products of the invention are useful for treating or prophylaxis of a condition in subject, which involves administering to the subject, an HAS and/or HYAL level-reducing or HAS and/or HYAL activity reducing effective amount of active molecule. The products of the invention have anabolic, hypertensive, gynaecological, neuroprotective, antianemic, cytostatic, anti-inflammatory, endocrinegen. and immunosuppressive activity. This sequence represents a peptide used in the method of the invention. NOTE: The specification describes SEQ ID NO 27-51 as nucleotide primers however the Sequence Listing represents the nucleotides in a three letter amino acid code, The
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                                                                                                                                                                                                                                                                                                                                         Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial cancer; inflammatory; immune; human secreted protein.
                                                                                                        represents the nucleotides in a three letter amino acid code nucleotide sequences have been made and are represented in {
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2002US-0406611P.
2002US-0406612P.
2002US-0406616P.
2002US-0406646P.
2002US-0406655P.
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2002US-0406655P.
2002US-0406655P.
2002US-0410948P.
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2002US-0410953P.
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2002US-0410961P.
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2002US-0411019P.
2002US-0411022P.
                                                                                                                                                      Similarity 20.0%;
2; Conservative C
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17-SEP-2002;
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hang H;
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MM, Kothakota S
ong JGP, Wu G,
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2002US-0411055P.
2002US-0411101P.
2002US-0411111P.
2002US-0411111P.
2002US-0411111P.
2003US-0463700P.
2003US-0463732P.
2003US-0467230P.
2003US-0485223P.
2003US-0486480P.
2003US-0485323P.
2003US-0486480P.
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2003US-0486480P.
2003US-0486481P.
2003US-0486481P.
2003US-04863370P.
2003US-0493370P.
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ilarity 20.0%; 1
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2002US-0411035P.
2002US-0411037P.
2002US-0411041P.
2002US-0411045P.
2002US-0411046P.
2002US-0411048P.
2002US-0411052P.
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such as proliferative
genetic, bacterial and
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The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antiinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
                                                                                                                                                                                                                                                                                    olecule for diagnosing, preventing or tre
ive (e.g. cancer), inflammatory, immune,
and viral diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthesis;
                                                                                                                                                                                                                                                                                                                              English.
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I MM, Kothakota S,
Wong JGP, Wu G,
                                                                                                                                                                                                         PRIME THERAPEUTICS INC.
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2003US-0467230P.

2003US-0471306P.

2003US-0472420P.

2003US-0472430P.

2003US-0476609P.

2003US-047661P.

2003US-0485218P.

2003US-0485218P.

2003US-0485224P.

2003US-0485224P.

2003US-048646P.

2003US-048646P.

2003US-048649P.

2003US-048649P.

2003US-048649P.

2003US-048649P.

2003US-048691P.

2003US-048690P.

2003US-0486960P.

2003US-04969371P.

2003US-0493370P.

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larity 20.0%;
Conservative 0
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such as proliferative (e.g
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sequence represents a
available on WIPOWEB
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Halenbeck RF,
Pierce K, Wa
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  02-MAY-2003;
19-MAY-2003;
22-MAY-2003;
22-MAY-2003;
09-JUN-2003;
09-JUN-2003;
08-JUL-2003;
08-JUL-2003;
08-JUL-2003;
14-JUL-2003;
15-JUL-2003;
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2002US-0406585P.
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2002US-0406688P.
2002US-0406611P.
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2002US-0406612P.
2002US-0406616P.
2002US-0406640P.
2002US-0406640P.
2002US-0406640P.
2002US-0410948P.
2002US-0410953P.
2002US-0410953P.
2002US-0411013P.
2002US-0411032P.
2002US-0411032P.
2002US-0411032P.
2002US-0411035P.
2002US-0411095SP.
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2003US-0463700P.
2003US-0467203P.
2003US-0467203P.
                                                                                                                     αn
                                                                                                                                        Antiinflammatory;
lammatory; immune;
                                                         standard; protein;
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cancer; inflammatory;
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17-SEP-2002;

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18-APR-2003;

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N-PSDB; ADL31229.
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17-SEP-2002;
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in CD-ROM
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                                                                                                                                        The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolat and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules has been determined. Primers for synthesising the full length cDNA are u for clarifying the function of the protein encoded by the cDNA. The length clones were obtained by construction of full length enriched libraries that were synthesised by the oligo-capping method. The price anable the production of the full length cDNA easily without any spenthuman cDNA of the invention. Note: The sequence data for this patent not form part of the printed specification, but was obtained in CD-Reformat directly from EPO
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T, Koga
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T, Koga
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3, Otsuki
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K, Kojima
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K, Kojima
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• T, Nagai
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2000JP-00118774.
2000JP-00183865.
2000EP-00114089.
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         08-JUL-1999; 99JP-00194486
11-JAN-2000; 2000JP-00118774
02-MAY-2000; 2000JP-00183765
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                                                                                    This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polypeptide sequence is a full length human protein of the invention.
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2002US-0406611P.
2002US-0406612P.
2002US-0406612P.
2002US-0406612P.
2002US-0406640P.
2002US-0406646P.
2002US-0406653P.
2002US-0406653P.
2002US-0406653P.
2002US-0410946P.
2002US-0410948P.
2002US-0410953P.
2002US-0410953P.
2002US-0410953P.
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2002US-0410958P.
2002US-0410958P.
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Antibacterial; Virucide;

Immunosuppressive, Ant. human secreted protein

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standard; protein; 144 AA
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2002US-0406585P.
2002US-0406588P.
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2002US-0406611P.
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2002US-0406612P.
2002US-0406612P.
2002US-0406612P.
2002US-0406616P.
2002US-0406655P.
2002US-0410946P.
2002US-0410949P.
2002US-0410953P.
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2002US-0410953P.
2002US-0410953P.
2002US-0410953P.
2002US-0411032P.
2002US-0411032P.
2002US-0411035P.
2002US-0411035P.
2002US-0411035P.
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2002US-0411046P.
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2002US-0411043P.
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2002US-0411019
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17-SEP-2002;
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encoding a polypeptide which is believed to be cytostatic,
antiinflammatory, immunosuppressive, antibacterial and virucida
composition and methods are useful for diagnosing, preventing a
treating diseases such as proliferative (e.g. cancer), inflamma
immune, metabolic, genetic, bacterial and viral diseases. The sequence represents a human secreted protein. The present sequence available on WIPOWEB and is not in the specification.
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Haishan L,
hang H;
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Wong JGP, Wu G,
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uch as proliferative (e.g. ca
enetic, bacterial and viral d
  2002US-0410961P.
2002US-0411019P.
2002US-0411022P.
2002US-0411023P.
2002US-0411032P.
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2002US-0411045P.
2002US-041101P.
2002US-0411045P.
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2002US-0411045P.
2002US-04110023P.
2002US-0467230P.
2003US-0467230P.
2003US-0467230P.
2003US-0467230P.
2003US-0472420P.
2003US-0472420P.
2003US-0472420P.
2003US-0485223P.
2003US-0485223P.
2003US-0485325P.
2003US-0485325P.
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2003US-04853370P.
2003US-0493370P.
2003US-0493573P.
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Pierce K, Wa
     17-SEP-2002;
17-SEP-2003;
18-APR-2003;
02-MAY-2003;
19-MAY-2003;
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The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a prophylaxis and treatment of pathological conditions resulting from a compound, such as a polypeptide, for the ability to bind a P. aeruginosa uncleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences AB067826-Components species using biochip technology. Sequences AB067826-Componence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                            Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary; inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell; aplastic anaemia; cancer; wound healing; gene therapy.
                                                                                                                                         Bush
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No. 3.5;
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Mismatches
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1. 169
/label= Unknown, OTHER
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                                                                                                                                                                                                                                                                    17897;
                                                                      98US-0074788P
98US-0094190P
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                                                                                                                                                                    WPI; 2003-615309/58.
N-PSDB; ABD02722.
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Misc-difference
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                                                                                                               GENOME
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                                                                      18-FEB-1998;
27-JUL-1998;
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                                            18-FEB-1999;
                22-APR-2003
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stic, bacterial and viral diseases.
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Haishan L,
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Kothakota S
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2003US-0463732P.
2003US-0467199P.
2003US-0467201P.
2003US-0467230P.
2003US-0471306P.
2003US-0471336P.
2003US-0472420P.
2003US-0472420P.
2003US-0472430P.
2003US-0476609P.
2003US-0485218P.
2003US-0485223P.
2003US-0485223P.
2003US-0486480P.
2003US-0486480P.
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2003US-0486491P.
2003US-0486491P.
2003US-048691P.
2003US-04869370P.
2003US-0493370P.
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ilarity 20.0%; 1
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18-APR-2003;
02-MAY-2003;
02-MAY-2003;
02-MAY-2003;
19-MAY-2003;
19-MAY-2003;
22-MAY-2003;
09-JUN-2003;
09-JUN-2003;
08-JUL-2003;
08-JUL-2003;
14-JUL-2003;
14-JUL-2003;
15-JUL-2003;
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15-JUL-2003;
08-AUG-2003;
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genetic,
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g MM, Kothakota S
Wong JGP, Wu G,
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2002US-0406655P.
2002US-0410646P.
2002US-0410946P.
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2002US-0410948P.
2002US-0410953P.
2002US-0410953P.
2002US-0410953P.
2002US-0410958P.
2002US-0410958P.
2002US-0410958P.
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2002US-0411032P.
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2002US-0411032P.
2002US-041103P.
2003US-04130P.
2003US-046720P.
2003US-0467230P.
2003US-0467230P.
2003US-046723P.
2003US-0485223P.
2003US-0485223P.
2003US-0485325P.
2003US-0486891P.
2003US-0485325P.
2003US-0486891P.
2003US-0483370P.
2003US-0493371P.
2003US-0493573P.
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 29-AUG-2002;

17-SEP-2002;

17-SEP-2003;

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17-SEP-2003;

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17-SEP-2003;

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18-APR-2003;

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14-JUL-2003;
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promoting
therapy
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О
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                                                                                                                                                                                        The invention relates to a novel isolated polynucleotide and the polypeptide. The molecules of the invention demonstrate antiinfl neuroprotective, antianaemic, cytostatic and vulnerary activitie be useful in preparing a composition for diagnosing or treating inflammatory, haematopoietic, immune, neurodegenerative or stem disorders, such as aplastic anaemia or cancer, as well as for prwound healing. The molecules may also be utilised during gene th procedures. The current sequence is that of a human therapeutic protein of the invention.
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Weng G,
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                                                                                                                                   New polynucleotide, useful in preparing a composition for diagnerating inflammatory, neurodegenerative or stem cell disordernaplastic anemia or cancer for promoting wound healing.
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Ghosh M,
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Wang J,
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2002US-0406579P.
2002US-0406588P.
2002US-0406608P.
2002US-0406611P.
2002US-0406611P.
2002US-0406616P.
2002US-0406616P.
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larity. 20.0%;
Conservative 'C
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                  30-SEP-2003; 2003WO-US030720
                                      2002US-0416186P
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                                                                            Asundi V, Ren F
Chen R, Zhao QA,
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antiinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
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                                                                         Length 171;
                                                                                         Indels
                                                                                                                                                                                                                                  Immunosuppressive; Anthuman secreted protein
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                                                                       Score 18; DB Pred. No. 3.5; 0; Mismatches
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2002US-040658BP.
2002US-040658BP.
2002US-040660BP.
2002US-0406611P.
2002US-0406611P.
2002US-0406612P.
2002US-0406612P.
2002US-0406612P.
2002US-0406616P.
2002US-0406655P.
2002US-0406655P.
2002US-0406655P.
2002US-0410948P.
2002US-0410948P.
2002US-0410948P.
2002US-0410958P.
2002US-0410958P.
2002US-0410959P.
2002US-0410959P.
2002US-0410959P.
2002US-0410953P.
2002US-0411032P.
2002US-0411032P.
2002US-0411032P.
2002US-0411032P.
2002US-0411033P.
                                                                                                                                                                                                                                  Cytostatic; Antiinflammatory; cancer; inflammatory; immune;
                                                                                                                                                                                                                                                                                                          2003WO-US026780
                                                                        Similarity 20.0%; 2; Conservative
                                                                                                                                                                  standard; protein;
                                                                                                                                                                                                                 Human secreted protein SEQ
                                                                                                                                                                                                   entry
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                                                                                                         CXXXXXXXC
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                                                          171
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17-SEP-2002;
                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                           -AUG-2003
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                                                                        Query Match
Best Local S
Matches
                                                                                                                         146
                                                          Sequence
                                                                                                                                                                  ADP30793
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ADP30793
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The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antiinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  olecule for diagnosing, preventing or treating distive (e.g. cancer), inflammatory, immune, metabolic, and viral diseases.
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Linnemann'
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, Haishan L,
Zhang H;
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Kothakota S
JGP, Wu G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 428pp;
2002US-0411046P.
2002US-0411052P.
2002US-0411052P.
2002US-0411055P.
2002US-041101P.
2002US-0411111P.
2002US-04111111P.
2003US-0463708P.
2003US-0463708P.
2003US-0463708P.
2003US-0467201P.
2003US-0467201P.
2003US-0467201P.
2003US-0467201P.
2003US-0472420P.
2003US-0472430P.
2003US-0476609P.
2003US-0476609P.
2003US-047661P.
2003US-0485218P.
2003US-0486891P.
2003US-0493370P.
2003US-0493370P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wong JGP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 20.0%; 2; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid molecule
such as proliferative (e.g
genetic, bacterial and vir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chu K,
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17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
18-APR-2003;
02-MAY-2003;
02-MAY-2003;
02-MAY-2003;
02-MAY-2003;
02-MAY-2003;
02-MAY-2003;
02-MAY-2003;
02-MAY-2003;
02-MAY-2003;
03-JUN-2003;
09-JUN-2003;
09-JUN-2003;
08-JUL-2003;
14-JUL-2003;
15-JUL-2003;
15-JUL-2003;
08-AUG-2003;
08-AUG-2003;
08-AUG-2003;
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Halenbeck RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 2
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The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
                                                                                                                                                                                                 New nucleic acid molecule for diagnosing, preventing or treating dise
such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
genetic, bacterial and viral diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibacterial
                                                                                                                                             PA, berry
                                                                                                                                               Behrens
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                                                                                                                                               Beaurang
Haishan L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aeruginosa polypeptide #8794
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                                                                                                                                               Hestir
                                                                                                                            PRIME THERAPEUTICS INC.
                                                                                                                                       Thu K, Lee E, Hestir
Huang MM, Kothakota
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191
                                                                                                                                                                                                                                               428pp;
2003US-0485218P.
2003US-0485223P.
2003US-0485224P.
2003US-0485325P.
2003US-0486446P.
2003US-0486480P.
2003US-0486991P.
2003US-0486960P.
2003US-0493341P.
2003US-0493370P.
2003US-0493370P.
2003US-0493370P.
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                                                                                                                                                                                                                                                                                                                                                                           100.0%;
larity 20.0%;
Conservative (
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98US-0094190P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-00252991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABO76619 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                               2804;
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                                                                                                                                                Chu K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
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2; Conserv
                                                                                                                                                                                                                                               SEQ ID NO
                                                                                                                                                                   Wang Y,
                                                                                                                                                                                                                                                                                                                                                         183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENO-) GENOME
                                                                                                                                                   Halenbeck RF,
Pierce K, Wai
  08-JUL-2003;
08-JUL-2003;
08-JUL-2003;
14-JUL-2003;
14-JUL-2003;
15-JUL-2003;
15-JUL-2003;
08-AUG-2003;
08-AUG-2003;
08-AUG-2003;
08-AUG-2003;
                                                                                                                              (FIVE-) FIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas
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27-JUL-1998
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Matches
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                                                                                                                                                                                                                                                 Claim 1;
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                                                                                                                                                Williams
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                                                            Virucide;
                                                             erial
                                                              mmunosuppressive; Ant
uman secreted protein
                                                               Immuno
human
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2002US-0406588P.
2002US-0406588P.
2002US-0406688P.
2002US-0406612P.
2002US-0406612P.
2002US-0406612P.
2002US-0406612P.
2002US-0406642P.
2002US-0410946P.
2002US-0410958P.
2002US-0411037P.
2002US-0411037P.
2002US-04110958P.
2003US-04110958P.
2003US-04110958P.
2003US-04110958P.
2003US-0411111P.
2003US-0467203P.
2003US-0467203P.
2003US-0471336P.
2003US-0471336P.
2003US-0476609P.
                                                               lammatory;
y; immune;
                                                                                                                                                     2003WO-US026780
                                           SEQ
                                            protein
                                                              Cytostatic; Antiinflam cancer; inflammatory;
                                            secreted
                                                                                                                                                                      29-AUG-2002;

17-SEP-2002;

17-SEP-2003;

17-SEP-2003;

17-SEP-2003;

17-SEP-2003;

17-SEP-2003;

18-APR-2003;

18-APR-2003;

19-MAY-2003;

19-MAY-2003;

19-MAY-2003;

19-MAY-2003;

19-MAY-2003;

19-MAY-2003;

19-MAY-2003;
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                          12-AUG-2004
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        ADP3 0806
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The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a pathological infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences AB067826-.

AB084396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.
                                                                sa polypeptide,
and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIAA0779; gene expression; inflammation; antiinflammatory; cancer;
proliferation; neoplasm; cytostatic; immune disorder; immunomodulator;
metabolic disorder; metabolic; viral infection; virucide; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  breast
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viral
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                                                              Novel isolated nucleic acid encoding Pseudomonas aeruginosa
useful as molecular targets for diagnostics, prophylaxis and
pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human KIAA0779 splice variant clone CLN00149041.a, protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                 ID NO 25365; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 3.6; ); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18;
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N-PSDB; ADZ56200, ADZ56231
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             WPI; 2003-615309/58
N-PSDB; ABD10190.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 191 AA;
                                                                                                                                 Disclosure; SEQ
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Gaps

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expression of the nucleic acid molecule), a recombinant host cell comprising the encoded proteins of the nucleic acid molecule), a recombinant host cell. Comprising the encoded proteins or the non-transmembrane (TW) regions of the proteins), a method of making a recombinant host cell, a method of making a recombinant host cell, a method of the proteins), a method of determining the proteins in a sample, a method of determining the nucleic acid molecule cited above in a sample, a method of determining the presence of a specific antibody to the polypeptide of (4) in a sample, an enthod of determining the presence of the polypeptide of (4) in a sample, a method of determining the presence of the polypeptide in a sample, an inclody sepecifically binding to and/or interfering with the biological activity of the nucleic acid molecule cited above (or the polypeptide or its biologically active freagment), a composition comprising a pharmaceutical carrier or excipient (and one or more active agents chosen from the nucleic acid molecule cited above, the vector, the polypeptide, and the antibody, an animal injected with one or more crown active agents (chosen from the nucleic acid molecule having at last 6 contiguous active agents (chosen from the nucleic acid molecule naving at last 6 contiguous compressing a nucleic acid molecule naving at last 6 contiguous nucleotides from the nucleic acid molecule naving at last 6 contiguous composition of making an antibody, and reagents occury out an immunoassay), a method of making an antibody, and reagents to carry out an immunoassay, a method of making an antibody, and reagents to carry out an immunoassay, a method of making an antibody, and reagents to carry out an immunoassay, that modulates the biological activity of the polypeptide, or antibody, and reagents to carry out an immunoassay, preferably kidney, cervical, squamous lung, ovarian, bladder, preferably kidney, cervical, squamous lung, ovarian, bladder, prevention and/or treatment of inflammacoutical carrier, breasent a 
                                                                                                                                       a
t
                                                                                                                 least one polynucleotide sequence (appearing as ADZ56196-ADZ56197, ADZ56199-ADZ56200, ADZ56226-ADZ56227 and ADZ56230-ADZ56231), sequences hybridizing to them under high stringency conditions, sequences having least 80% sequence identity to them, their complements or biologically active fragments. The nucleic acids are splice variants or biologically
                                                                                                                                                                                                                                                                                                                                      Active fragments. The nucleic acids are splice variants of the human KIAA0779 gene, encoding transmembrane domain protein(s). Also included are a double-stranded isolated nucleic acid molecule comprising the nucleic acid molecule cited above, a vector comprising the isolated nucleic acid molecule cited above (and a promoter that regulates the expression of the nucleic acid molecule), a recombinant host cell comprising the nucleic acid molecule cited above, an isolated polypepting the nucleic acid molecule cited above, an isolated polypepting the nucleic acid molecule cited above, an isolated polypepting the nucleic acid molecule cited above, an isolated polypepting the nucleic acid molecule cited above, an isolated polypepting the nucleic acid molecule cited above, an isolated polypepting the nucleic acid molecule cited above, an isolated polypepting the nucleic acid molecule cited above, an isolated polypepting the nucleic acid molecule cited above, an isolated polypepting the nucleic acid molecule cited above, an isolated polypepting the nucleic acid molecule cited above, an isolated polypepting the nucleic acid molecule cited above and acid molecule cited above acid molecule cited above acid molecule cited acid mo
                                        English.
                                          18; 121pp;
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                                               SEO
                                          11;
                                                  Claim
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Gaps .. 0 Length 214; Indels .; æ 9 DB 3.7; ed. No. 3.7; Mismatches 18; Pred . 0 100.08; larity 20.0%; Conservative Similarity 2; Conserv Query Match Best Local

214 AA;

Sequence

.; 0

182 10 CXXXXXXXC CAAAAAAAC --1 173 dd ò

RESULT 15

Antibacterial; Immunosuppressive; Anti human secreted protein. #1688. Z standard; protein; 228 Human secreted protein SEQ ID Cytostatic; Antiinflammatory; cancer; inflammatory; immune; (first entry) 12-AUG-2004 ADP30921 ADP30921 NX K

Virucide;

Homo sapiens

treating diseases ne, metabolic,

nucleic acid molecule for diagnosing, preventing or treas proliferative (e.g. cancer), inflammatory, immune, ic, bacterial and viral diseases.

2004-348438/32

WPI;

nucleic

Wang Y,

Williams LT, Halenbeck RF, Pierce K, War

SEQ ID NO 2919; 428pp; English.

Claim 1;

genetic,

such New

Û

PA, Behrens D Linnemann T;

Chu K, Lee E, Hestir K, Beaurang | Huang MM, Kothakota S, Haishan L, ng Y, Wong JGP, Wu G, Zhang H;

PRIME THERAPEUTICS INC.

FIVE

(FIVE-)

08-AUG-2003; 2003US-0493577P

The

acid molecule

The present sequence is

composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.

The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antiinflammatory, immunosuppressive, antibacterial and virucidal composition and methods are useful for diagnosing, preventing and

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2002US-0406576P.
2002US-0406585P.
2002US-0406588P.
2002US-0406608P.
2002US-0406608P.
2002US-0406612P.
2002US-0406652P.
2002US-0410953P.
2002US-0410953P.
2002US-0410953P.
2003US-046720P.
2003US-046720P.
2003US-046720P.
2003US-046720P.
2003US-046720P.
2003US-046720P.
2003US-046720P.
2003US-0486480P.
2003US-0486480P.
2003US-0486891P.
2003US-0486891P.
2003US-0493370P.
2003US-0493370P.
                           003WO-US02678
                                       29-AUG-2002;
17-SEP-2002;
17-SEP-2003;
18-APR-2003;
19-AAY-2003;
02-MAY-2003;
19-MAY-2003;
02-MAY-2003;
02-MAY-2003;
02-MAY-2003;
09-JUN-2003;
09-JUN-2003;
09-JUN-2003;
09-JUL-2003;
15-JUL-2003;
08-JUL-2003;
08-JUL-2003;
08-AUG-2003;
08-AUG-2003;
              -APR-2004
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Gaps

.. 0

Indels

а Э

., score 18; DB E . Pred. No. 3.8; 0; Mismatches

100.0%; illarity 20.0%; 1 Conservative 0

Similarity 2; Conserv

Query Match Best Local S Matches 2

Sequence 228 AA;

10

CXXXXXXXC

63

CATAAATTAC

54

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2006, 08:54:55

7

Search completed: May Job time: 113.791 secs

Length 228;

8;

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5.1.7
Biocceleration Ltd
  GenCore version (c) 1993 - 2006
               Copyright
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model 3 using protein search, OM protein

2, 2006, 08:47:12 Мау Run on:

; Search time 18.1395 Seconds
 (without alignments)
53.043 Million cell updates/sec

US-10-046-922-33

CXXXXXXX 10 score: Sequence: Title: Perfect

, Gapext BLOSUM62 Gapop 10.0 Scoring table:

0.5

residues 283416 seqs, 96216763 Searched: hits satisfying chosen parameters: o F number Total

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

\*:08 PIR Database

piri: \*
pir2: \*
pir4: \* H 0 M 4

Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being paand is derived by analysis of the total score distribution.

### SUMMARIES

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RESULT

GB:AE001963; GB:AE000513; N

R.J.

J.D.; Dodson, T.; Zalewski,

radiodurans

hypothetical protein - Deinococcus radiodurans (strain R1)
C; Species Deinococcus radiodurans
C; Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004
C; Accession: E7543
R; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodsor K; White, O.; Eisen, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A; Reference number: A75250; MUID:20036896; PMID:10567266
A; Tatus: preliminary
A; Molecule type: DNA
A; Residues: 1-480 <WHI>A; Residues: 1-480 <WHI>A; Residues: uNIPROT:Q9RV87; UNIPARC:UPI0000C18A8; GB:AE001963; GB:AE00CA; GGenetics:
A; Gene: DR1142
A; Map position: 1
C; Superfamily: Deinococcus radiodurans hypothetical protein DR1142

able elongat	ypothetical 30.9	bable elongati	othetical	robable yop tra	bable elicitor	othetical prot	d-box-contai	othetical pro	othetical p	52 protein hom	polysaccharid	robable lipopoly	le glutamat	ypothetical pro	cerol-3-phosph	
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30	31	32	1 E	34	35	36	37	- 60 - C1	6 M	0 4	41	42	4.3	4 4	45	

## ALIGNMENTS

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UNIPARC:UPI000013B90A; EMBL:Z48755; NID:g736296;
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                                                             #text_change 09-Jul-2004
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hypothetical protein YMR206w - yeast (Saccharomyces cerevisiae)
hypothetical protein YMR325.07
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 30-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 09-C;Accession: S59448
R;Odell, C.; Bowman, S.
submitted to the EmBL Data Library, March 1995
A;Reference number: S59441
A;Accession: S59448
A;Molecule type: DNA
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A;Residues: 1-313 < ODE>
A;Cross-references: UNIPROT:Q03695; UNIPARC:UPI000013B90A; EMBL:Z46
A;Experimental source: strain AB972
C;Genetics:
A;Gene: MIPS:YMR206w
A;Cross-references: SGD:S0004819
A;Map position: 13R
                                                                                                                                                                                                                                                                                                                                                  Length 313;
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-33

-10-046-922

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hypothetical protein KOIC8.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23167
R;Sims, M.
Submitted to the EMBL Data Library, April 1995
A;Reference number: Z19702
A;Accession: T23167
A;Accession: T23167
A;Accession: T23167
A;Accession: T23167
A;Accession: T23167
A;Accession: T23167
A;Accession: Caenorical type: DNA
A;Molecule type: DNA
A;Molecule type: Lanslated from GB/EMBL/DDBJ
A;Residues: 1-389 < WIL>
A;Residues: 1-389 < WIL>
A;Coss-references: UNIPROT:Q21081; UNIPARC:UP1000080155; EMBL:Z49068; PIDN:CAA88855.
A;Coss-references: Clone K01C8
C;Genetics:
A;Gene: CESP:K01C8.2
A;Map position: 2
A;Introns: 54/2; 146/3; 208/3; 283/1; 379/3
                                                                                                                                    GB: AE008688; PIDN: AAL43776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A; Reference number: A97359; MUID:21608551; PMID:11743194
A; Reference number: A97359; MUID:21608551; PMID:11743194
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-388 < KUR>
A; Residues: 1-388 < KUR>
A; Cross-references: UNIPROT:Q8UBQ6; UNIPARC:UPI00000D2014; GB:AE007869; PIDN:AAK88508
C; Genetics:
A; Gene: AGR C_5073
A; Map position: circular chromosome
C; Superfamily: Methanobacterium cobalamin biosynthesis protein D
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Markelz,
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   C58
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Engineer Agrobacterium tumefaciens PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S.; Miller, N.; Blanchard, M.; Qurollo, M.; Doughty, D.; Scott, C.; Lappas, C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cobalamin biosynthetic protein cbiD (PA2908) [imported] - Agrobacterium tumm(C; Species: Agrobacterium tummefaciens
C; Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C; Accession: C97694
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Science 294, 2323-2328, 2001
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 A; Title: The Genome of the Natural Genetic Engineer Agriculary
A; Reference number: AB2577; MUID:21608550; PMID:11743193
A; Accession: AB2920
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-376 < KUR>
A; Cross-references: UNIPROT:Q8UBQ6; UNIPARC:UPI0000164772; GB:AE00
A; Experimental source: strain C58 (Dupont)
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: Methanobacterium cobalamin biosynthesis protein D
C; Superfamily: Methanobacterium cobalamin biosynthesis
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C; Species: Cymbidium mosaic virus
C; Date: 21-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2
C; Accession: JC4082
R; Ryu, K.H.; Yoon, K.E.; Park, W.M.
Gene 156, 303-304, 1995
A; Title: Cloning and sequencing of a cDNA encoding the coat protein of a A; Reference number: JC4082; MUID:95278762; PMID:7758973
A; Reference number: JC4082, MUID:95278762; PMID:7758973
A; Residues: JC4082
A; Molecule type: mRNA
A; Residues: 1-220 < RYU>
A; Residues: 1-220 < RYU>
A; Residues: The authors translated the codon GTG for residue 161 as Leu
C; Superfamily: potato virus coat protein
C; Keywords: coat protein
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                                                                                                                                                                                                                                               hypothetical 20.6K protein - Lymantria dispar nuclear polyhedrosis N; Alternate names: hypothetical protein 4
C; Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-C; Accession: JQ1560
R; Bjornson, R.M.; Rohrmann, G.F.
J. Gen. Virol. 73, 1499-1504, 1992
A; Title: Nucleotide sequence of the polyhedron envelope protein gen A; Reference number: PQ0339; MUID:92300345; PMID:1607868
A; Accession: JQ1560
A; Molecule type: DNA
A; Residues: 1-194 < BJO>
A; Cross-references: UNIPROT:P36868; UNIPARC:UPI000017A7BF; DDBJ:D10
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Pred. No. 1.6;
0; Mismatches 8; Indels
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J.; Kutyavin, T
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       Query Match
Best Local
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19; Science 283, 2103, 1999; a:
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A;Description: involved in protein folding and assembling/disassembling of I
C;Superfamily: bcr protein
C;Keywords: ATP; mitochondrion; molecular chaperone; stress-induced protein
F;1-23/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F;24-634/Product: heat shock protein 70, mitochondrial #status predicted <W
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 21-Jun-200
C;Accession: D87803
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for invest A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/A;Note: published errata appeared in Science 283, 35, 1999; Science 283, A;Accession: D87803
A;Accession: D87803
A;Accession: D87803
A;Cross-references: UNIPARC:UPI000016B639; GB:chr_I; PIDN:AAB96754.1; PID: C;Genetics:
A;Gene: bli-4D
A;Map position: 1
C;Superfamily: kexin; subtilisin homology
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S09118
G surface protein 168 - Paramecium primaurelia
C;Species: Paramecium primaurelia
C;Species: Paramecium primaurelia
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_chang
C;Accession: S09118
R;Prat, A.
J. Mol. Biol. 211, 521-535, 1990
A;Title: Conserved sequences flank variable tandem repeats in A;Reference number: S09118; MUID:90172419; PMID:2308165
A;Accession: S09118
A;Molecule type: DNA
A;Residues: 1-2704 <PRA>
A;Residues: 1-2704 <PRA>
A;Residues: 1-2704 <PRA>
A;Genetics:
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C;Superfamily: G surface protein
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0; Mismatches
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illarity 20.0%;
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Matches 2; Conservative
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Glask-type molecular chaperone precursor, mitochondrial - Leishmania major
Glask-type molecular chaperone precursor, mitochondrial - Leishmania major
N.Alternate names: heat shock protein 70-related protein; mitochondrial stress
C;Species: Leishmania major
C;Species: Leishmania major
C;Species: Leishmania major
C;Species: Jo-Leo-1997 Headler Sider 
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N,Alternate names: Disterase 4
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-C;Accession: T37314
R;Thacker, C.; Peters, K.; Srayko, M.; Rose, A.M.
Genes Dev. 9, 956-971, 1995
A;Title: The bli-4 locus of Caenorhabditis elegans encodes structurally A;Reference number: Z21679; MUID:95293228; PMID:7774813
A;Accession: T37314
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-570 <THA>
A;Residues: 1-570 <THA>
A;Cross-references: UNIPARC:UPI000016B8E1; EMBL:L29440; NID:g459702; PII
C;Genetics:
A;Gene: bli-4
A;Map position: I
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Pred. No. 2.3;
0; Mismatches
                     Pred, No. 2; ; Mismatches
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Cross-references: UNIPARC:UPI000016BF1C;
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                      Similarity 20.0%; 2; Conservative
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: E70531
R;Color, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Conor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID: 98295987; PMID: 9634230
A;Reference number: A70500; MUID: 98295987; PMID: 9634230
A;Reference number: A70500; MUID: 98295987; PMID: 9634230
A;Residues: 1-85 <COL>
A;Title: Door, B.A.
A;Residues: 1-85 <COL>
A;Title: Davies preferences: UNIPROT: 007207; UNIPARC: UPI00000C14DC; GB: Z96072; GB: AL123456; NID: GGenetice: Rv2706c
A;Genetice: Rv2706c
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hypothetical protein Vng1598h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: F84312
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, Jung, K.H.; Alam, M.; Freitas, T.
Cibeithauser, B.; Keller; K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl, Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L.A;Alatile: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: F84312
A;Relerence number: DNA
A;Residues: 1-71 <STO>
A;Cross-references: UNIPROT:Q9HPK1; UNIPARC:UPI0000063920; GB:AE004437; NID:g10581076; C;Genetics:
A;Gene: VNG1598H
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C;Species: Arabidopsis thaliana (%)
C;Species: Arabidopsis thaliana (%)
C;Date: 15-Jul-1995 #sequence_revision 03-Nov-1995 #text_change C;Accession: S51479; S43176
R;Gosti, F.; Bertauche, N.; Vartanian, N.; Giraudat, J.
Mol. Gen. Genet. 246, 10-18, 1995
A;Title: Abscisic acid-dependent and -independent regulation of A;Reference number: S51478; MUID:95124290; PMID:7823904
A;Accession: S51479
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                                   UNIPARC:UPI000000BF21; EMBL:X78585; submitted to the EMBL Data Library,
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C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_chang
C;Accession: A71249
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazak
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: A71249
A;Accession: A71249
A;Accession: A71249
A;Cross-references: UNIPROT:057986; UNIPARC:UPI000062D66; GB:A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence; PH0248
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A; Molecule type: mRNA
A; Residues: 1-104 <GOS>
A; Cross-references: UNIPROT:Q39084; UNIPAR(
A; Note: the nucleotide sequence was submitt
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A; Gene: Di21
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                     Copyright
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2006, 7 May Run on:

08:38:27 ; Search time 113.256 Seconds (without alignments) 62.295 Million cell updates/sec

US-10-046-922-33 18 score: Title: Perfect so Sequence:

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Scoring table:

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2166443 seqs, 705528306 residues Searched:

of hits satisfying chosen parameters: Total number

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_05.80:\*
.: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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Swiss-Prot entry is copyright. It is produced through a collaboration
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
NCBI_TaxID=180454;
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STRAIN=S288c / AB972;
MEDLINE=97313268; PubMed=9169872;
Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S.V., Whitehead S., Barrell B.G.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome
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Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which preliminary data.
EMBL; AAAB01008807; EAL41760.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   281;
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"Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
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01-NOV-1997 (Rel. 35, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Hypothetical 35.0 kDa protein in PFK2-HFA1 intergenic OrderedLocusNames=YMR206W; ORFNames=YM8325.07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                           update)
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Last annotation
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Mismatches
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01-FEB-2005 (TrEMBLrel. 29, L
01-FEB-2005 (TrEMBLrel. 29, L
ENSANGPO0000027669 (Fragment)
ORFNames=ENSANGG00000000023;
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01-FEB-2005
01-FEB-2005
01-FEB-2005
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STRAIN=PEST;
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Q03695;
01-NOV-1997
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           Trypanosoma brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
NCBI_TaxID=5691;
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                                                                              STRAIN=GUTat10.1;
Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hanr Shallom J., Hou L., Djikeng A., Feldblyum T., Hostetler J., Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J. Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S. Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A. Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Cul
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Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry preliminary data.

EMBL; AAAB01008847; EAA06779.3; -; Genomic_DNA.
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to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
STRAIN=GUTat10.1;
El-Sayed N.M., Khalak H., Adams M.D.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                   STRAIN=GUTat10.1;
Haas B., Blandin G., El-Sayed N.;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ
EMBL; AC008146; AAX80300.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                  Score 18; DB 2
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Q7PRQ7 ANOGA PRELIMINARY;
Q7PRQ7;
Q1-MAR-2004 (TrEMBLrel. 26, Las
01-MAR-2004 (TrEMBLrel. 26, Las
01-MAR-2004 (TrEMBLrel. 26, Las
ENSANGP0000001657 (Fragment).
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20.0%;
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The Anopheles gambiae
"Anopheles gambiae re-
Submitted (APR-2002) t
                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 263 AA; 2
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269 AA;
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Anophelinae; Anoph
NCBI_TaxID=180454;
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    ORFNames=Tb927.6
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Insecta; Pterygota; ra; Culicoidea; Culicidae;

Last sequence update)
Last annotation update)

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The Anopheles gambiae Sequence Committee;
"Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
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Submitted (APR-2004) to the EMBL/GenBank/DDBJ dat
-!- CAUTION: The sequence shown here is derived !
EMBL/GenBank/DDBJ whole genome shotgun (WGS)
preliminary data.
EMBL; AAAB01008807; EAA04378.2; -; Genomic_DNA.
 01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update
01-MAR-2004 (TrEMBLrel. 26, Last annotation update
01-MAR-2004 (TrEMBLrel. 26, Last annotation update
ENSANGP0000000383 (Fragment).
ORFNames=ENSANGG00000007023;
Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta
Neoptera; Endopterygota; Diptera; Nematocera; Cu.
Anophelinae; Anopheles.
NCBI TaxID=180454;
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2; Conservative (
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TIGR; DR1142; -.
Complete proteome; F
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STRAIN=PEST;
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Best Local
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Oryza gativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                           Length 313
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Nuclear (By similarity).
1; -; Genomic_DNA.
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genomic DNA, chromosome
    and
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3 6 Poly-Ser.
146 149 Poly-Gln.
246 252 Poly-Ser.
313 AA; 35018 MW; 9D92BFDE982577F0
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  between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There are as long as its content is in no way modific
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Last annotation u
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DR4 ORYSA
Q6ZDR4 ORYSA PRELIMINARY; PRT; 357 AA
Q6ZDR4;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence up
05-JUL-2004 (TrEMBLrel. 27, Last annotation
Putative transcription factor Myb protein.
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                                                                                    Genomic_DNA
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                                                  Joban Josephania Joban Joban Joban Joban Joban Joban Jacobaromyces Ct. SGD; S00004819; YMR206W. Complete proteome; Hypothetic COMPBIAS Jacobaromes Jacobards Sequence Sacrametric Company Jacobards Sequence Jacobards Sequence Jacobards Ja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sasaki T., Matsumoto T., Yamamo "Oryza sativa nipponbare (GA3) g clone: P0481F05.";
Submitted (NOV-2001) to the EMB.
-!- SUBCELLULAR LOCATION: Nuclei EMBL; AP004376; BAD09322.1; -; (HSSP; Q03237; 1A5J.
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Score 18; DB Pred. No. 0.52 0; Mismatches

; 0

CRC64;

384376DDF431BEC0

entry which is

databases.

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NUCLEOTIDE SEQUENCE.

STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;

MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571, white O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Noffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  radioresistant bacterium Deinococcus
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49364 MW;
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Deinococcaceae; Deinococcus.
NCBI_TaxID=1299;
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20.0%;
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Science 286:1571-1577(1999).
EMBL; AE001963; AAF10716.1;
PIR; E75433; E75433.
                                           01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2003 (TrEMBLrel. 24, Hypothetical protein DR1142, orderedLocusNames=DR1142;
Q9RV87 DEIRA PRELIMINARY;
Q9RV87;
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Best Local Similarity
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TRANSMEM 6
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae
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S.W.,
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.D.

A Robards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length hu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL o the European Bioinformatics Institute. There are no restrictiuse as long as its content is in no way modified and this state
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The German cDNA consortium;
Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
   Indels
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sequences.";
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10-MAY-2005 (Rel. 47, Last annotation update)
Transmembrane and coiled-coil domains protein
Name=TMCC1; Synonyms=KIAA0779;
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EMBL; BC039859; AAH39859.1; -; mRNA.
EMBL; CR749206; CAH18064.2; -; mRNA.
Ensembl; ENSG0000172765; Homo sapie:
HGNC; HGNC:29116; TMCC1.
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    Conservative
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16-OCT-2001 (Rel. 40, C
10-MAY-2005 (Rel. 47, I
10-MAY-2005 (Rel. 47, I
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The bacterial blight pathogen of rice.";

Nucleic Acrisl Bes. 33:577-586(2005).

B. BMBL; AE013598; AAW74484.1; -; Genomic_DNA.

GO; GO:0005622; C:intracellular; IEA.

GO; GO:0001111; F:nucleoside-triphosphatase activity; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0000355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR001993; AAA ATPase.

InterPro; IPR001940; TPR.

InterPro; IPR011717; TPR. 4.

Ream; PF00156; GerE; 1.

Ream; PF00156; TPR. 4; 1.

Ream; PF00151; TPR. 4; 1.

Ream; PF001307; HTH LuxR; 1.
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Kim H.,
Seo J.-S.
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
NCBI_TaxID=64187;
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PubMed=15673718; DOI=10.1093/nar/gki206;
Lee B.-M., Park Y.-J., Park D.-S., Kang H.-W. Park I.-C., Yoon U.-H., Hahn J.-H., Koo B.-S.
Park H.-S., Yoon K.-O., Kim J.-H., Jung C.-H.
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0.77;
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Last annotation
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Pred. No. 0.77
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Q5H317;
10-MAY-2005 (TrEMBLrel. 30, Last sequen
10-MAY-2005 (TrEMBLrel. 30, Last sequen
10-MAY-2005 (TrEMBLrel. 30, Last annota
Transcriptional regulator.
Name=acoK; OrderedLocusNames=XOO1230;
 Potential.
Potential.
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SM00421; HTH LUXR; 1.
SM00028; TPR; 3.
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Submitted (NOV-2004) to the
EMBL; AY814691; AAW26423.1;
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                                                                           PRELIMINARY;
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NCBI_TaxID=9606;
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SEQUENCE 12
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05DCN3;
10-MAY-2005
10-MAY-2005
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Submitted
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Irie R.,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophy
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooi
Triticeae; Hordeum.
NCBI_TaxID=4513;
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                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
STRAIN=Friedlin;
Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J. Smith D., Collins M., Fosker N., Harris D., Oliver K., O'Neil Saunders D., Seeger K., Warren T., Rajandream M., and Barrell Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; CT005259; CAJ03791.1; -; Genomic_DNA.
SEQUENCE 1061 AA; 113930 MW; 2C69385D06371DCD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; InterPro; IPR002197; HTH_Fis.
                                                                                                                                                                                                                                                                                                                                                Length 1061;
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Baldwin A., Harwood J.L., Machray G.C., Francis D., Rogers Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ419772; CAD11963.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52;
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                                              13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Kinesin heavy chain, putative.
ORFNames=LmjF20.0640;
Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomat
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. 22, Last sequence update)
. 26, Last annotation updat-
-transferase (Fragment).
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Baldwin A.;
"The effect of thiocarbamate herbicides and the barley and wild oats.";
Thesis (2001), Department of Cardiff School of Buniversity, Cardiff, United Kingdom.
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52
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13-SEP-2005 (T)
Kinesin heavy
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homi
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K., Isogai
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GO; GO:0004672; F:protein kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation;
InterPro; IPR000719; Prot_kinase.
Pfam; PF00069; Pkinase: 1.
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
ATP-binding; Kinase; Nucleotide-Dinding; Transferase SEQUENCE 128 AA; 14116 MW; D30AC8C668621B0C CRC6
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FLJ25437.
Homo sapiens (Human)
update)
on update)
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                                                                       Trematoda; Schistosoma
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awamura M.
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                                                                                                                                                                                 sequences of Schistosoma
to the EMBL/GenBank/DDBJ o
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TISSUE=Testis;
Kawakami B., Sugiyama A., Takemoto M., Suzuki
Nakagawa K., Mizuno S., Morinaga M., Kawamura
Irie R., Otsuki T., Sato H., Nishikawa T., Nag
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   Last sequence up
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Pred. No. 1.8;
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Submitted (OCT-2001) to the EMBL/GenBar
EMBL; AK058166; BAB71697.1; -; mRNA.
Ensembl; ENSG00000178093; Homo sapiens
                         Hypothetical protein.
Schistosoma japonicum (Blood fluke)...
Eukaryota; Metazoa; Platyhelminthes;
Schistosomatoidea; Schistosomatidae;
NCBI_TaxID=6182;
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TO 50-JUL-2004 (TrEMBLrel. 27, Last sequence update)

TO 50-JUL-2004 (TrEMBLrel. 27, Last sequence)

TO 60-JUL-2004 (TrEMBLrel. 27, Last sequence)

TO 70-Za activa (japonica cultivar-group)

TO 70-Za setiva (Japonica cultivar-group)

TO 70-Za setiva nipponbare (A3) genomic DNA, chromosome 8, BAC

TO 70-Za setiva nipponbare (A3) genomic DNA.

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Search completed: May 2, 2006, 08:46:46 Job time : 116.256 secs

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/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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US-10-10-2524-1851

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US-10-141-759-49 US-10-140-805-49	10-140	US-10-184-644-167	US-10-184-634-16	US-10-146-731-15	US-10-140-472-15	US-10-141-761-15	US-10-142-885-15	US-10-158-790-15	US-10-137-871-15	US-10-140-923-15	US-10-141-756-15	US-10-141-7	4 US-10-140-805-153	4 US-10-140-864-153
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# ALIGNMENTS

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APPLICANT: Watkins, Jeffry D.
APPLICANT: Huse, William D.
APPLICANT: Huse, William D.
APPLICANT: Vasserot, Alain P.
APPLICANT: Smith, Eric P.
TITLE OF INVENTION: Methods of Optimizing Antibody Variable Region Binding Affinity FILE REFERENCE: AME-08122
CURRENT APPLICATION NUMBER: US/10/697,399
CURRENT FILING DATE: 2003-10-30
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin version 3.2
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APPLICANT: Larry W. Kwak
APPLICANT: Arya Biragyn
TITLE OF INVENTION: VIRAL CHEMOKINE-ANTIGEN FUSION PROTEINS
FILE REFERENCE: 14014.0381U2
CURRENT APPLICATION NUMBER: US/10/380,927
CURRENT FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: PCT/US01/29075
PRIOR FILING DATE: 2001-09-17
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
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Mismatches
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Application US/10697399
10. US20040162413A1
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Publication No. US20040110165A1
GENERAL INFORMATION:
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ilarity 20.0%;
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                                                                                                                                                                                                                                                                                                                      Sequence
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    Sequence 10, Application Publication No. US20 GENERAL INFORMATION:
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US-10-380-927-7
                                                                                                                                                                                                                                                               SEQ ID NO 10
LENGTH: 33
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                                                                       of Artificial Sequence
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; Sequence 231, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TRE
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                ; DB 2.3;
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Mismatches
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CURRENT APPLICATION NUMBER: US/10/296,115

CURRENT FILING DATE: 2002-11-18

PRIOR APPLICATION NUMBER: US09/488,725

PRIOR FILING DATE: 2000-01-21

PRIOR APPLICATION NUMBER: US09/552,317

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 1478

SEQ ID NO 800
                                                                                                                            Score 18;
                                                                       Description of Arti
Synthetic Construct
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; Sequence 800, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
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SEQ ID NO 7
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial S
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LENGTH: 339
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US-10-287-436A-216

Sequence 216, Application US/10287436A

Publication No. US20050202421A1

GENERAL INFORMATION:

APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER

TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF

TITLE OF INVENTION: RHEUMATOID ARTHRITIS

FILE REFERENCE: 10872.514696

CURRENT APPLICATION NUMBER: US/10/287,436A

CURRENT FILING DATE: 2002-10-31

PRIOR APPLICATION NUMBER: US 60/336,220
                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.
TITLE OF INVENTION:
NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSCOM
SEQ ID NO 51398
LENGTH: 356
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OTHER INFORMATION: RIBOKINASE SIGNATURE
OTHER INFORMATION: number PR00990B, p-ve
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RE: FastSEQ for Windows Version
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Sequence 51398, Application US/
Publication No. US20050196754A1
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OTHER INFORMATION: Xaa
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LENGTH: 405
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Kovalic, David
Zhou, Yihua
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Cao, Yongwei
Wu, Wei
Boukharov, Ar
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nes 2; Conser
 Publication No. US20
GENERAL INFORMATION:
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US-10-287-
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US-10-287-436A-206

Sequence 206, Application US/10287436A

Publication No. US20050202421A1

GENERAL INFORMATION:

APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER

TITLE OF INVENTION: RHEUMATOID ARTHRITIS

FILE REFERENCE: 10872.514696

CURRENT FILING DATE: 2002-10-31

PRIOR APPLICATION NUMBER: US 60/336,220

PRIOR FILING DATE: 2001-10-31

NUMBER OF SEQ ID NOS: 1446

SOFTWARE: FastSEQ for Windows Version 4.0
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  Pred. No. 3.5
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                                                                                                  RESULT 7
US-10-424-955A-28
; Sequence 28, Application US/10424955A
; Publication No. US20040014658A1
; Publication No. US20040014658A1
· GENERAL INFORMATION:
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Vavon, Avner
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US-10-287-436A-257
; Sequence 257, Ap.
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ENGTH: 429
YPE: PRT
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
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; Sequence 271, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
    APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
    TITLE OF INVENTION: RHEUMATOID ARTHRITIS
    TITLE OF INVENTION: RHEUMATOID ARTHRITIS
    FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
    PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 271
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APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TRI
TITLE OF INVENTION: RHEUMATOID ARTHRITIS
FILE REFERENCE: 10872.514696
CURRENT APPLICATION NUMBER: US/10/287,436A
CURRENT FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: US 60/336,220
PRIOR FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 1446
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 257
LENGTH: 465
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US-10-437-963-162631
; Sequence 162631, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
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; ORGANISM: Homo Sapien
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LENGTH: 647
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e 539,
                                            APPLICANT:
APPLICANT:
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Pred. No. 3
CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID.NO 162631 LENGTH: 598
                                                                                          Clone ID: PAT MRT4530
                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/791,279
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/184,715
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/184725
PRIOR FILING DATE: 2000-02-24
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ER: 60/184,690
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APPLICATION NUMBER: 6
FILING DATE: 2000-02-
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Linda S.
i, Luis
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FILING DATE: 2000
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                                                                  ORGANISM: Oryza sativa FEATURE:
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nes 2; Conser
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Parodi,
                                                                                         ; OTHER INFORMATION:
US-10-437-963-162631
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TITLE OF INVENTION:
FILE REFERENCE: 0
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-09-791-279-86
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APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES. AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                                                                                                                                                                                                                                                                         See File Wrapper
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CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrap NUMBER OF SEQ ID NOS: 612
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CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
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US-10-184-634-539
; Sequence 539, Application US/10184634
; Publication No. US20030068684A1
; GENERAL INFORMATION:
Sequence 539, Application US/10184644 Publication No. US20030044930A1 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 539
LENGTH: 647
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                                                      Baker, Kevin P
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RESULT 15
US-09-374-046A-20
Sequence 20, Application US/09374046A
Sequence 20, Application US/09374046A
Publication No. US20030096951A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: Lavallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Evans, Cheryl
APPLICANT: Steininger David
APPLICANT: Steininger II, Robert J.
APPLICANT: Steininger II, Robert J.
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Ganetics Institute, Inc.
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Pred. No. 3.8;
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
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; LOCATION: (604)
US-09-374-046A-20
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US-11-096-56 US-11-217-99 US-11-096-56	-10-315-002-24 -10-131-826A-2 -10-973-115B-2 -10-137-873A-2	US-10-152-37 US-11-290-1 US-11-217-9 US-11-217-9	4-487-26 5-883-26 5-888-26 5-888-26 5-899-26	S-11-145-405B S-11-241-631- -10-194-487-4	US-10-195-888-451 US-10-195-889-451   US-11-241-631-7   US-11-241-631-3
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TITLE OF INVENTION: Division
FILE REFERENCE: 6769*2
CURRENT APPLICATION NUMBER: US/11/174,341
                                                                                                                                                                                                                                                                                                                                                                                  Length 25;
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Sequence 24, Application US/11217995
; Sequence 24, Application US/11217995
; Publication No. US20060073142A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Chan
APPLICANT: Lawren Wu
; TITLE OF INVENTION: ANTI-FC-GAMMA RIIB RECEF;
; FILE REFERENCE: P1935R1
; CURRENT APPLICATION NUMBER: US/11/217,995
; CURRENT FILING DATE: 2002-08-12
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 24
; LENGTH: 25
                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: sequence is synthesized 11-217-995-24
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5. US20060031967A1
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Best Local Similarity
Matches 2; Conser
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APPLICANT: Slade, Ar APPLICANT: Madisen, APPLICANT: Madisen, APPLICANT: Comai, I
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APPLICANT: National Institutes of Health
ITILE OF INVENTION: Catalytic Domains of
TITLE OF INVENTION: and Acceptor Specificitie
TITLE OF INVENTION: and Methods.for Their Use
FILE REFERENCE: 1662.001US1
CURRENT APPLICATION NUMBER: US/11/178,230
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Pred. No. 0.0; Mismatches
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APPLICANT: Ensrud, Kathy M
TITLE OF INVENTION: CRISP POLYPEPTIDES AS CO
TITLE OF INVENTION: CAPACITATION
FILE REFERENCE: 110.01860101
CURRENT APPLICATION NUMBER: US/10/515,868
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: 60/383,628
PRIOR FILING DATE: 2002-05-28
PRIOR FILING DATE: 2002-05-28
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/US2004/000470
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SOFTWARE: FastSEQ for Windows Version
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Publication No. US20050282729A1
GENERAL INFORMATION:
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               Conservative
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APPLICATION NUMBER:
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US-11-178-230-10
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US-10-515-868-8
Similarity 2; Conserv
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RE: PatentIn
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NUMBER OF SEO ID N
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APPLICANT: Lawren Wu
TITLE OF INVENTION: ANTI-FC-GAMMA RIIB RECEPTOR ANTIBODY AND USES THES
FILE REFERENCE: P1935R1
CURRENT APPLICATION NUMBER: US/11/217,995
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: US 60/606,851
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 40
SEQ ID NO 37
LENGTH: 370
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US-11-079-463-10130

Sequence 10130, Application US/11079463

Publication No. US20060073161A1

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELYTILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: PATHOO-03DIV2

CURRENT APPLICATION NUMBER: US/11/079,463

CURRENT FILING DATE: 2005-03-14

PRIOR APPLICATION NUMBER: US 60/128,705

PRIOR FILING DATE: 1999-04-09
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Pred. No. 9.9e-05;
; Mismatches 8;
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Pred. No. 0.00018;
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; OTHER INFORMATION: sequence is synthesized
US-11-217-995-37
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PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 09/540,209
PRIOR FILING DATE: 2000-04-04
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; Sequence 37, Application US/11217995
; Publication No. US20060073142A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Chan
; APPLICANT: Robert Shields
; APPLICANT: Lawren Wu
2005-07-01
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ORGANISM: Artificial sequence
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LENGTH: 407
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CURRENT FILING DATE: 20 NUMBER OF SEQ ID NOS: 21 SOFTWARE: Patentin Ver. SEQ ID NO 161 LENGTH: 36
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                                                                           TYPE: PRT
ORGANISM: Plant
                                                                                                        US-11-174-341-161
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Sequence 97, Application US/10195889 Publication No. US20060074227A1 GENERAL INFORMATION: APPLICANT: Baker, Kevin P.
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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NUMBER OF SEQ ID NOS: 612
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Chen, Jian
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US-10-195-888-97
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US-10-195-883-97
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LENGTH: 1894
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APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gorney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: DATE: 2002-07-12
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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Mismatches
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R APPLICATION NUMBER: 60/063121

R APPLICATION NUMBER: 60/063486

R FILING DATE: 1997-10-24

R FILING DATE: 1997-10-21

R APPLICATION NUMBER: 60/063540

R FILING DATE: 1997-10-28

R APPLICATION NUMBER: 60/063541

R APPLICATION NUMBER: 60/063541

R FILING DATE: 1997-10-28

R APPLICATION NUMBER: 60/063541

R FILING DATE: 1997-10-28

R FILING DATE: 1997-10-28

R FILING DATE: 1997-10-28
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US-10-195-883-97
; Sequence 97, Application US/10195883
; Publication No. US20060073544A1
; GENERAL INFORMATION:
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ilarity 20.0%;
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Goddard, Audrey
                               CTATATATAC 1368
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audre
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ORGANISM:
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APPLICANT: APPLICANT: APPLICANT: APPLICANT: Ban, James
APPLICANT: Pan, James
APPLICANT: Wartanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Alang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C323
CURRENT APPLICATION NUMBER: US/10/195,883
CURRENT FILING DATE: 2002-07-15
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 97
LENGTH: 1894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CANT: Zhang, Zemin
OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
OF INVENTION: ACIDS ENCODING THE CAME
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Pred. No. 0.00027
; Mismatches
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APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBR?
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C324
CURRENT APPLICATION NUMBER: US/10/195, 888
CURRENT FILING DATE: 2002-07-15
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Publication No. US20060073545A1
GENERAL INFORMATION:
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, ORGANISM: Homo Sapien
US-10-194-487-525
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Publication No. US2(
GENERAL INFORMATION
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; Sequence 5, Application US/11241631
; Publication No. US20060020115A1
; GENERAL INFORMATION:
    APPLICANT: Bamber, Bruce
    APPLICANT: Jorgensen, Erik
    TITLE OF INVENTION: Methods Related Thereto
    FILE REFERENCE: 21101.0009U4
; TITLE OF INVENTION: Methods Related Thereto
    FILE REFERENCE: 21101.0009U4
; CURRENT APPLICATION NUMBER: US/11/241,631
; CURRENT FILING DATE: 2005-09-30
    PRIOR FILING DATE: 2002-05-24
    PRIOR FILING DATE: 1999-11-08
; PRIOR FILING DATE: 1999-11-08
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.1
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                                               APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C329
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red. No. 0.00027;
Mismatches 8;
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Pred. No. 0.00027
; Mismatches
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CURRENT FILING DATE: 2002-07-15
Prior Application removed - See File Wrapp
NUMBER. OF SEQ ID NOS: 612
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; Sequence 525, Application US/10194487
; Publication No. US20060074226A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
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larity 20.0%;
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Chen, Jian
Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J
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US-10-195-889-97
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ENGTH: 1894
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APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C312
CURRENT APPLICATION NUMBER: US/10/194,487
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No. 0.00034;
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C323
CURRENT APPLICATION NUMBER: US/10/195,883
CURRENT FILING DATE: 2002-07-15
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R FILING DATE: 2002-01-15

R APPLICATION NUMBER: 60/059263

R FILING DATE: 1997-09-18

R APPLICATION NUMBER: 60/059266

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R APPLICATION NUMBER: 60/062250
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R APPLICATION NUMBER: 60/063540
R FILING DATE: 1997-10-28
R APPLICATION NUMBER: 60/063541
R FILING DATE: 1997-10-28
R APPLICATION NUMBER: 60/063544
R FILING DATE: 1997-10-28
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APPLICATION NUMBER: 60/063120
FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/063121
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APPLICATION NUMBER: 60/063486
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TYPE: PRT ORGANISM:
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APPLICANT: Goddard, Austin L.
APPLICANT: Godwski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C324
CURRENT APPLICATION NUMBER: US/10/195,888
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CURRENT APPLICATION NUMBER: US/10/195,888
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SEQ ID NOS: 612
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LENGTH: 4440
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APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
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US-10-195-889-525
Sequence 525, Application US/10195889
Publication No. US20060074227A1
GENERAL INFORMATION:
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US-10-195-888-525
; Sequence 525, Application US/10195888
; Publication No. US20060073545A1
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CURRENT APPLICATION NUMBER: US/10/195,889
CURRENT FILING DATE: 2002-07-15
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#### STIMMARTER

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### ALIGNMENTS

haemangioma; Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antiidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangion diabetes; PDGF; platelet derived growth factor. ID NO:35. 10 AA SEO ABP53932 standard; peptide; entry) binding peptide (first 09-JAN-2003 ABP53932; VEGFR-3 RESULT 1 ABP53932

WO200257299-A2 Homo sapiens. 25-JUL-2002 Synthetic. 

CANCER RES 16-JAN-2002; 2002WO-IB000099 2001US-0262476P (LUDW-) LUDWIG INST C (LICN ) LICENTIA LTD. 17-JAN-2001;

Ή Kubo Koivunen E, Χ, Alitalo

2002-691521/74 WPI;

activity useful for VEGFR-3 a New isolated peptide that inhibits VEGF-C and VEGF-D, I diagnosing, evaluating, treating disorders mediated by such as cancer and diseases of neovascularization.

Claim 13; Page 80; 149pp; English.

and of The present invention describes an isolated peptide (I) that binds to a inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity

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the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver; spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, or skin, head and neck, oesophagus, bone, marrow or blood, and diseases neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
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the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovskin, head and neck, oesophagus, bone, marrow or blood, and diseases neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the present invention
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g, treating disorders mediated
seases of neovascularization.
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5. .7
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larity 100.0%;
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gnosing, evaluating, trea
h as cancer and diseases
                                                                                                                                                                                                                                                                   peptide;
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                      VEGFR-3 binding
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such as cancer
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diagnosing, e
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Synthetic.
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the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ov skin, head and neck, oesophagus, bone, marrow or blood, and diseases neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a VEGFR-3 binding peptide, which is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                 receptor;
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5. 1.1e+02;
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Pred. No. 1.1e
2; Mismatches
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ilarity 60.0%;
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ilarity 60.0%;
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                                                                                                                                                                                                                                                                                           standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                composition
                                                                                                                                                           cytostatic; cancer; gene therapy; DGI-2; DGI-5; DGI-7; DGI-9; Hras; leptin; VEGF; vascular endothelial growth factor receptor; VEGF-R1; VEGF-R2; VEGF-R3; FLT1; FMS-related tyrosine kinase 1; FLK1; KDR; kinase insert domain protein receptor; EGFR; epidermal growth factor; FGFR1; fibroblast growth factor;
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Pred. No. 16;
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Tiel-binder peptide of the invention
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Goldstein N;
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                                                                                                                                       Cancer-related Tie-1-binder
                                                             peptide;
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 CGFW-AVWGC
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6; Conserv
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                                                              ADC99638 standard;
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Prendergast J,
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                        Evaluating comprising peptide lig
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         enic milk;
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        blood; plasma; transgericulatory system.
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                                                                                                                                                                        New polypeptides, useful as binding molecules for detecting, purifying immunoglobulin Fc-region polypeptides present in a for regulating or preventing an antibody response.
                                                                                                                                                                                                                                                                                                                                          Length 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour; human.
                                                                                                                                       JC,
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                                                                                                                                       Ransohoff
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         region; binding; whole blood; half-life; stability; circula
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Pred. No.
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                                                                                                                                                                                                             152pp; English
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                                                                                     2002WO-US012492
                                                                                                                                                                                                                                                                                                                                         63.9%;
ilarity 66.7%;
Conservative
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         Immunoglobulin Fc ; antibody response;
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                                                                                                                                                                                                            Page 76;
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                                                                                                                                         Wu Q,
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                                                                                                                                                                                                                                                                                                                           Sequence 17 AA;
                                                   WO200286070-A2
                                                                                                      18-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DYAX-) DYAX
                                                                                     18-APR-2002;
                                  Unidentified
                                                                                                                        (DYAX-) DYAX
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                                                                    31-OCT-2002
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                                                                                                                                        Rondon IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADJ50741;
                                                                                                                                                                                                             Claim 3;
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                                                                                                                                                                                                                                                                                                          peptide
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The invention relates to a method of evaluating sample by providing a soluble serum protein (I), one or more compounds physically associated with (I), and a (I)-binding agent that comprises a peptide that specifically binds to (I), allowing the (I)-binding agent to bind to (I) to form a complex including one or more compounds physically associated with (I), separating the complex from one or more components of the sample, and evaluating one or more of the physically associated compounds. The sample comprises blood or serum, or is obtained from a biopsy. The sample may also be obtained from a tumour or a region within solupsy. The method is useful for detecting modulators that modulate interaction of serum protein-binding compound and serum protein sequence represents a serum albumin-binding peptide identified using the method of the invention.
                                                                                                     separated
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                                              by forming complex compounds using is, which is separat
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                       uating sample comprising soluble serum protein by rising serum protein and physically associated con ide ligand that specifically binds with proteins, evaluated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xue A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human EST derived amino acid sequence SEQ ID NO:743.
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Mismatches
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                                                                                                                                                                                          278; 191pp; English
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Pred. No. 15
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D, Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADM87650 standard; protein; 136 AA
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28-MAR-2002; 2002US-00112944.
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ilarity 66.7%;
Conservative
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Ghosh MJ, Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                          Disclosure; SEQ ID NO
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WPI; 2004-082161/08.
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N-PSDB; ADM87432.
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generating polymucleotides encoding chimeric or fusion profeshs and heterologous protein sequences. The polymucleotides can be used to express recombinant protein for analysis, characterisation or therapeutic use; as markers for tissues in which the corresponding protein is professored; as markers or tags to identify chromosomes or to map related gene chromosome markers or tags to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridise and discover genes, related DNA sequences as a source of information to derive PCR primers for genetic fingerprinting; as a probe to subtract-out known sequences in the process of discovering other novel polymucleotides; for sequences in the process of discovering other novel polymucleotides; for actachment to a gene chip or other support, including for examination of expression patterns; to raise antiportein antibodies using DNA immunisation techniques; and as an antigen protein antibodies using DNA immunisation techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. The polymucleotides and polypeptides can also be used as nutritional sources or supplements, e.g. as a protein or amino acid supplement, as a carbon source, as an itrogen source or as a source of carbohydrates. The polymucleotides and polypeptides can also be used treat closure of non-fortusing woulds, for the generation and regeneration of tissues, for gut protection or regeneration and regeneration of itssues, for graft versus host disease. The compositions can also be used to treat inflammatory conditions (e.g. arthritis, inflammatory bowel disease). sepsis, rheumatoid arthritis, diabetes mellitus type 1 or graft versus host disease. The present sequence from the present inflammatory conditions (e.g. arthritis, and sequence from the present invention. N. B. The sequences for this patent were obtained from the prevence of the provest of the provest of the provest
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                                                                                                                                                                                                                                                                                                                                                                     The present invention describes an isolated polynucleotide (I): comprising a nucleotide sequence selected from SEQ ID NO:1-244; which encodes a polypeptide with biological activity, where the polynucleotide hybridises to (I) under stringent hybridisation or has greater than 99% sequence identity with (I). (I) has respected antibacterial, immunosuppressive, antidiabetic and antirheumatic activities, and can be used in gene therapy. (I) can be used for generating polynucleotides encoding chimeric or fusion proteins
         useful for treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·.
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New isolated polynucleotides and polypeptides, useful for trescancer, lung or liver fibrosis, arthritis, inflammatory bowel Crohn's disease, rheumatoid arthritis, diabetes mellitus type versus host disease.
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Pred. No. 89;
1; Mismatches
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ilarity 60.0%;
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                                                                                                                                                                                                                                                                                                               The invention relates to a method of modulating insulin activity in mammalian cells by administering a peptide that binds the insulin receptor (IR). A composition containing a peptide, optionally expressed from gene therapy vectors, that binds to Site 1 of IR and an insulin agonist are useful for treating diabetes. Also, peptides that are useful for treating diabetes. Also, peptides that are useful for treating insulin-like growth factor-1 (IGF-1) receptor are useful for treating insulin-like growth factor (IGF)-sensitive tumours (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1 receptor agonists are useful for treating neurological diseases, including stroke and diabetic neuropathy. The peptides are also useful screening for compounds that bind to IR or IGF-1 receptor, potential therapeutics and research reagents. AAU88034-AAU90957 represent IR and/or
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Ostergaard
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                                                                                                      This invention describes novel cDNA sequences (A) highly expressed in normal uterine tissue which can have anticancer and cytostatic activity and can be used for gene therapy. (A) are used (i) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of uterine cancer (ii) directly for treating this form of cancer (including expression fine gene therapy vectors) and (iii) for generation of specific antibodies.

(A) are identified by assembling ESTs (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTs from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. AAY59838-Y59892 represent protein fragments encoded the human uterine tissue derived cDNA fragments represented in AAZ41328
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25-OCT-2001;
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or agane an which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; a scrivity; (11) a culture comprising strains in which the strains is present in a culture or collection of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for extent or collular proliferation to isolate candidate molecules for rational and an organism or for extensional and an organism of an organism or extension and extensional and an organism or extension of an organism or extensional and an organism or extensional and an organism or extensional and an organism or extension of an organism or extension or an organism or extension or extensional and an organism or extension or extensional and an organis
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  useful for identifying proteins or s required for cellular proliferation for rational drug discovery programs.
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The present invention describes a method for detecting a stress that alters a functional interaction of a low density lipoprotein (LDL) receptor binding protein (I) with an LDL receptor interaction domain (II). The method involves introducing a predetermined stress into a system which provides a stress-biased physical interaction of (I) with an LDL receptor interaction of (I), where in the absence of the stress, the system provides an unbiased interaction of (I), where a difference between BI and UI indicates that the stress alters the interaction of (I) and (II). (I) is selected from caress alters the interaction of (I) and (II). (I) is selected from SEMCAP-1, JIP-1, PSD-95, JIP-2, Talin, OMP25, CAPON, PIP4,5 Kinase, Na channel brain 3, Mintl, ICAP-1 and APC subunit 10. The method is useful for detecting a stress that alters functional interaction of LDL receptor binding polypeptide with LDL receptor interaction domain. The method is useful for detecting and modulating signal transduction through LDL receptors. ABB04778 to ABB04909 represent LDL receptor binding proteins which are used in the exemplification of the present invention
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                                                                                              Detecting stress that alters interaction of LDL receptor binding polypeptide with LDL receptor interaction domain, comprises detailference in stress-biased and unbiased interaction of peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen binding molecule; Fc receptor; B-cell marker; CD20; antibody engineering; B-cell depletion; B cell lymphoma; cytos hematological disease; immune disorder; neoplasm; heavy chain;
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receptor binding affinity and effector function, useful for
agnosing, preventing or treating B-cell proliferative disorders,
aluding B cell lymphoma.
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                                                                                    The specification describes antigen binding molecules with incr receptor binding affinity and effector function. These antigen molecules may have modified glycosylation, and are especially s for human B-cell marker CD20. The invention is useful for diagn preventing or treating disorders or diseases treatable by B-cel depletion, such as B cell lymphoma. The present sequence represanting molecule of the invention.
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The specification describes antigen binding molecules with increased Foreceptor binding affinity and effector function. These antigen binding molecules may have modified glycosylation, and are especially specific for human B-cell marker CD20. The invention is useful for diagnosing, preventing or treating disorders or diseases treatable by B-cell depletion, such as B cell lymphoma. The present sequence represents an antigen binding molecule of the invention.
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Search time 18.1395 Seconds (without alignments) 53.043 Million cell updat

US-10-046-922-35 score: Title: Perfect

CGYWLTIWGC Scoring table: Sequence:

Gapext BLOSUM62 Gapop 10.0

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96216763 residues 283416 segs, Searched: 283416 chosen parameters: hits satisfying οĘ number Total

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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pland is derived by analysis of the total score distribution.

### SUMMARIES

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## ALIGNMENTS

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GB:AB001339; N
June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E.; Nakamura, Y.; Miyajima, N
Watanabe, A.; Yamada, M.; Yasu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the unicellular cyanobacterium Synechocyst
RESULT 1
S76385
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
C;Species: Synechocystis sp.
C;Species: Synechocystis sp.
C;Bate: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S76385
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; M
C; Accession: S76385
B;Kaneko, T.; Watanabe, A.; Asamizu, E.; Nakamura, Y.; M
NA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium S
S.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76385
A;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                09-Jul-2004
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Gaps ö Length 218 Indels 7 Score 46; DB 2 Pred. No. 8.2; 1; Mismatches 63.9%; ilarity 66.7%; Conservative Query Match Best Local Similarity Matches 6; Conser

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σ CGYWLTIWG | | | | : | | CGYWVGRWG 73 g 8

ATP-dependent helicase [imported] - Yersinia pestis (strain C092)

C; Species: Yersinia pestis
C; Species: Yersinia pestis
C; Species: Yersinia pestis
C; Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004
C; Accession: AD0412
R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. Ribarkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. Simmonds, M.; Skelton, J.; Stevens, R.M.; Davis, P.; Dougan, G. il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell Nature 413, 523-527, 2001
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Accession: AD0412
A; Catesion: AD0412
A; Status: preliminary
A; Accession: AD0412
A; Status: 1-828 < XCR.>
A; Catesious: 1-828 < XCR.>
A; Cossious: 1-828 < XCR.>
A; Cross references: UNIPROT: Q82BL4; UNIPARC: UPI00000CDA15; GB: AL590842; PIDN: CAC92624.
C; Superfamily: ATP-dependent RNA helicase, HrpB type

45; Score 62.5%; Query Match

Length 828

5;

DB

shown

2

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shown;
A;Status: nucleic acid sequence not shandlecule type: DNA
A;Residues: 1-72 <DON>
A;Cross-references: UNIPROT:Q05245; UNA;Note: the nucleotide sequence was such a;Genetics:
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62.5%;
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5; Conservative
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C;Species: Rattus norvegicus (Norway rat)
C;Accession: T42388
C;Accession: T42388
R;Dib-Hajj, S.D.; Tyrrell, L.; Black, J.A.; Waxman, S.G.
A;Reference number: Z22149; MUID:98338024; PMID:9671787
A;Reference number: Z22149; MUID:98338024; PMID:96898
A;Reference number: Z22149; MUID:98338024; PMID:98880; PMID:98880
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C;Species: Aplysia californica (California sea hare)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2
C;Accession: T30902
R;Dyer, J.R.; Johnston, W.L.; Castellucci, V.F.; Dunn, R.J.
DNA Cell Biol. 16, 347-356, 1997
A;Title: Cloning and tissue distribution of the Aplysia Na+ channel alph A;Reference number: Z20929; MUID:97238630; PMID:9115644
A;Reference number: Z20929; MUID:97238630; PMID:9115644
A;Accession: T30902
A;Statuus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1993 < DYE>
A;Cross-references: UNIPROT:P90670; UNIPARC:UPI000007A0B4; EMBL:U66915;
C;Superfamily: sodium channel protein
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C;Species: Mycobacterium phage L5
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-
C;Accession: $30980
R;Donnelly-Wu, M.K.; Jacobs Jr., W.R.; Hatfull, G.F.
Mol. Microbiol. 7, 407-417, 1993
A;Title: Superinfection immunity of mycobacteriophage L5: applications A;Reference number: $30949; MUID:93211283; PMID:8459767
                                  5;
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Pred. No. 1.6e+02;
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Pred. No. 1.3e+02;
3; Mismatches 1
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      Pred. No. 37; ; Mismatches
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59; PII
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K.; Yeh, 1
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multidrug resistance-associated protein homolog MLP-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42216
R;Hirohashi, T.; Suzuki, H.; Ito, K.; Ogawa, K.; Kume, K.; Shimizu, T.; Sugiyama, Y.
Mol. Pharmacol. 53, 1068-1075, 1998
A;Title: Hepatic expression of multidrug resistance-associated protein-like proteins may; Reference number: 222081; MUID:98279126; PMID:9614210
A;Reference number: 222081; MUID:98279126; PMID:9614210
A;Residues: 1-1502 AHIR>
A;Experimental source: strain Sprague-Dawley; liver
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      NID:g15859
December 1
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      UNIPARC:UPI000013 submitted to the
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lone C16C8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               permease [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-c;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-c;Shoression: E90446
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; X;She, Q.; Singh, R.K.; Sensen, C.W.; Wan der Oost, J. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: E90446
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-419 <KUR>
A;Genetics:
C;Genetics:
A;Genetics:
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                                                                                                #text_change
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R; Waterston, R.; Le, T.T.; Gattung, S.
A; Reference number: Z20617
A; Reference number: Z20617
A; Reference number: Z20617
A; Accession: T29407
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-referra
                                                                    C; Species: Pyrococcus sp.
C; Date: 07-Feb-1996 #sequence_revision 19-Apr-1996 #text_C; Date: 07-Feb-1996 #sequence_revision 19-Apr-1996 #text_C; Accession: PC4117
R; Rashid, N.; Morikawa, M.; Imanaka, T.
Gene 166, 139-143, 1995
A; Title: An abnormally acidic TATA-binding protein from a A; Reference number: JC4514; MUID: 96105215; PMID: 8529878
A; Accession: PC4117
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: UNIPARC: UPI000017AEAF; DDBJ: D50018
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                                                                                                                                                                                                    protein from
PMID:8529878
                      (fragment
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Pred. No. 79;
2; Mismatches
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                       replication protein homolog - Pyrococcus sp. N;Alternate names: hypothetical 391 protein
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larity 62.5%;
Conservative
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C; Genetics:
A; Gene: CESP:C16C8.2
A; Map position: 2
A; Introns: 68/2; 179/3;
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5; Conserv
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Best Local S
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A; Title: The complete genome of the hyperthermophilic bacterium Aquifex aeol A; Reference number: A70300; MUID:98196666; PMID:9537320

A; Accession: F70439

A; Molecule type: DNA

A; Molecule type: DNA

A; Residues: 1-620 <AQF>
A; Cross-references: UNIPROT:067544; UNIPARC:UPI000005667F; GB:AE000747; NID: A; Experimental source: strain VF5

C; Genetics:
A; Genetic
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 ATP-bindi
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-
C;Accession: F70439
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.V.
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                                                        Length 1502
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  resistance protein cMOAT2;
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                                                   Score 42; DB 2;
Pred. No. 1.7e+02
; Mismatches
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A; Introns: 31/3; 66/2; 114/3; 149/2; 232/2; 284/1
A; Note: T1008.150
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Pred. No. 94;
2; Mismatches
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Pred. No. 61;
3; Mismatches
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ilarity 50.0%;
Conservative
                                                      58.3%;
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Best Local Similarity 60.0%;
Matches 6; Conservative
    human multidrug
                                                                              Similarity 71.55; Conservative
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964 GYWLSLW 970
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CSFVVSIWGC
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     C; Superfamily:
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Best Local S
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Best Local S
Matches 6
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Job time
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c;Species: Mus musculus (house mouse)
c;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
c;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
c;Accession: A55138
K;Felipe, A.; Knittle, T.J.; Doyle, K.L.; Tamkun, M.M.
J. Biol. Chem. 269, 30125-30131, 1994
A;Title: Primary structure and differential expression during development and pregn
A;Reference number: A55138; MUID:95074002; PMID:7982916
A;Reference number: A55138
A;Reference number: A55138
A;Residues: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1681 <FEL>
A;Residues: 1-1681 <FEL>
A;Residues: 1-1681 <FEL>
C;Superfemily: sodium channel protein
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                                                                                                                                                                                                                             sodium channel alpha subunit - long-tailed hamster (fragment)
C;Species: Cricetulus longicaudatus (long-tailed hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change C
C;Accession: I48108
R;Lalik, P.H.; Krafte, D.S.; Ciccarelli, R.B.
Am. J. Physiol. 264, 803-809, 1993
A;Title: Characterization of endogenous Sodium channel gene expre A;Reference number: I48107
A;Reference number: I48108
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-200 <RES>
A;Cross-references: UNIPROT:Q60464; UNIPARC:UPI00000E60A9; GB:M87
C;Genetics:
A;Gene: chol
C;Superfamily: sodium channel protein
C;Keywords: duplication
                                                                                                                                                                                                                                                                          change
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                                   Length 739;
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myeloperoxidase homology
                                Score 41; DB 2; Le
Pred. No. 1.3e+02;
; Mismatches 3;
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Pred. No. 3.1e+02;
2; Mismatches 2;
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A45380
sodium channel protein alpha chain hNav2.1 - human C; Species: Homo sapiens (man)
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 C; Accession: A45380
R; George Jr., A.L.; Knittle, T.J.; Tamkun, M.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40.5; D. Pred. No. 50; 2; Mismatches
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Local Similarity 54.5%;
nes 6; Conservative
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Best Local Similarity 54.5%;
Matches 6; Conservative
 myeloperoxidase;
                                                    Similarity 60.06; Conservative
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 C; Superfamily:
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Proc. Natl. Acad. Sci. U.S.A. 89, 4893-4897, 1992
A;Title: Molecular cloning of an atypical voltage-gated sodium channel expressed in huma; Reference number: A45380; MUID: 92279233; PMID:1317577
A;Reference number: A45380
A;Reference number: A45380
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1682 <GEO>
A;Cross-references: UNIPROT:Q01118; UNIPARC:UPI00001279D2; GB:M91556; NID:g189046; PID: A;Experimental source: heart
A;Experimental source: heart
C;Superfamily: sodium channel protein
C;Superfamily: sodium channel protein
C;Superfamily: sodium membrane protein; phosphoprotein; sodium channel; voltage-ga
C;Superfamily: sodium channel protein
C;Creywords: glycoprotein; membrane protein; phosphoprotein; sodium channel; voltage-ga
C;Superfamily: Sodium channel protein
C;Creywords: glycoprotein; membrane protein; phosphoprotein; sodium channel; voltage-ga
C;Creywords: glycoprotein; membrane protein; phosphoprotein; phosphop
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GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
                Copyright
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- protein search, using sw model OM protein

2, 2006, 08:38:27 ; Search time 113.256 Seconds (without alignments) 62.295 Million cell updates/sec May Run on:

US-10-046-922-35 72 1 CGYWLTIWGC 10 score: Title: Perfect so Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 segs, 705528306 residues

2166443 Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt\_05.80:\*
.: uniprot\_sprot:\*
: uniprot\_trembl:\* .. ..

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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ω	4,	59.7	9	7	Q6H022_FREDI	fremyella
0		59.7	Н	~	Q57Z63_9TRYP	trypanoso
10	43	٠. ص	$\sim$	7	Q4QID2_LEIMA	leishmania
. 41		· .	N	~	Q74JK6_LACJO	lactobaci
12		`. G	S	~	Q59NK9_CANAL	candida
13	43	О	0	7	Q6C574_YARLI	yarrowia
₹ #	43	59.7	520	7	Q4XP68_PLACH	plasmodium
15	43	О	4	~	Q8DKD6_SYNEL	synechoc
16		О	m	7	Q8H2N7_ORYSA	oryza
17		ς. Ο	1084	7	Q7WY20_PSEAE	psendo
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31	42	8	-	Н	RBL_NITVU	59613 nit

Q8vq84 nitrosospir Q9xd76 nitrobacter Q9xd77 nitrobacter Q8t6h2 dictyosteli Q54ek2 dictyosteli Q9r1s7 mus musculu Q9r1s7 mus musculu Q9r1s7 pomo sapien Q8n1z5 homo sapien Q5t2n8 homo sapien Q5t2n8 homo sapien	Q8zzss encerococcu Q9m030 arabidopsis Q6cbe4 yarrowia li
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# ALIGNMENTS

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Best Local Similarity
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01-MAR-2002
01-MAR-2004
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ATP-binding;
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STRAIN=T / IAM 14863;

STRAIN=T / IAM 14863;

PubMed=15383646; DOI=10.1093/nar/gkh830;

PubMed=15383646; DOI=10.1093/nar/gkh830;

Nocimura K., Ikeda H., Hattori M., Beppu T.;

Morimura K., Ikeda H., Hattori M., Watsuji T.,

Morimura K., Ikeda H., Hattori M., Watsuji T.,

Morimura K., Ikeda H., Hattori M., Watsuji T.,

Go, GO:000422; F:metalloendopeptidase activity; IEA.

GO, GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR002886; Peptidase M238.

R Pfam; PF01551; Peptidase M23; I.

Complete proteome; Copper; Hypothetical protein; Metal-binding;
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Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
Berriman M., Florens L., Janssen C.S., Pain A., Christophides G
James K., Rutherford K., Harris B., Harris D., Churcher C.,
Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
Bidwell S.L., Rajandream M.A., Carucci D.J, Yates J.R., Kafatos
Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.
"A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses.";
Science 307:82-86(2005).
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                                                                                                                                                      13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein.
ORFNames=PC103204.00.0;
Plasmodium chabaudi.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry preliminary data.
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Last annotation update)
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Pred. No. 55;
0; Mismatches
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Bacteria, Actinobacteria; Symbiobacterium
NCBI_TaxID=2734;
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SEQUENCE 173 AA; 21349 MW;
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8; Conservative
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                                                                                                                           Q4YICE_PLACH PRELIMINARY;
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Complete proteome; Coppei
Oxidoreductase.
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73 CGYWVGRWG
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NCCLECTIDE SEQUENCE.

STRAIN=CO-92 / Biovar Orientalis;

STRAIN=CO-92 / Biovar Orientalis;

MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;

MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;

MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

A Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,

Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Genome sequence of Yersinia pestis, the causative agent of plague.";

Nature 413:523-527(2001).

R EMBL; AD0412.
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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TIGR01970; DEAH box HrpB; 1.
1g; Complete profeome; Helicase; Hydrolase.
828 AA; 91983 MW; 3A11F88835D5E583 CRC64;
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(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 26, Last annotation updat
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Score 45; DB
Pred. No. 1.3e
1; Mismatches
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GO:0008026; F:ATP-dependent helicase.
GO:0016787; F:hydrolase activity; IEA.
GO:0003676; F:nucleic acid binding; I
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No.
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InterPro; IPR011545; DEAD/DEAH N.

InterPro; IPR010225; DEAH box HrpB.

InterPro; IPR001650; Helicase C.

InterPro; IPR007502; Helicase dom.

Pfam; PF00270; DEAD; 1.

Pfam; PF00270; DEAD; 1.

Pfam; PF00271; Helicase C; 1.

Pfam; PF00271; Helicase C; 1.

SMART; SM00487; DEXDC; 1.
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Enterobacteriaceae; Yersinia
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58.3%;
       62.5%;
85.7%;
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Q66EF6 YERPS
ID Q66EF6 YERPS PRELIMINARY;
AC Q66EF6;
DT 25-OCT-2004 (TrEMBLrel. 28,
DT 25-OCT-2004 (TrEMBLrel. 28,
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                                                                                                                                                                                                                                                                         OBZBL4 YERPE PRELIMINARY;
Q8ZBL4;
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                                Similarity 85. 6; Conservative
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CGYWLTI - - WGC
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GO:0005261; F:ca
GO:0005248; F:vo
GO:0006812; P:ca
GO:0006814; P:ca
           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                   Similarity 7; Conserv
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GO:0016020;
                    STRAIN=91001;
PubMed=15368893
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                                                                                    NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=IP32953 / Serotype I;

NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=IP32953 / Serotype I;

Pubmed=1536858; DOI=10.1073/pnas.0404012101.

Regala W.M.; Gaorgescu A.M.; Vergez L.M.; Land M.L.; Motin V.L.;

Regala W.M.; Georgescu A.M.; Vergez L.M.; Land M.L.; Motin V.L.;

Regala W.M.; Georgescu A.M.; Vergez L.M.; Land M.L.; Modigue C.;

Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.

A Derbise A.; Hauser L.J.; Garcia E.;

Toomparison With Yersinia pseudotuberculosis.";

Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).

EMBL; BX936398; CAH19977.1; -; Genomic_DNA.

GO; GO:0008026; F:ATP binding; IEA.

RO; GO:0008264; F:ATP binding; IEA.

RO; GO:00016787; F:hydrojase activity; IEA.

RO; GO:00016787; F:hydrojase activity; IEA.

RINTERPRO; IPR001410; DEAD.

RINTERPRO; IPR001502; Helicase_dom.

RINTERPRO; IPR001502; Helicase_dom.

REAM; PF00271; Helicase_dom.

REAM; PF00271; Helicase_C; 1.

RESP; PIRSF005496; ATP_hel_hrpB; 1.

SWART; SM00487; DEEAD:

RESPRESSORT; MORAPE; MATP_hel_hrpB; 1.
                                               ŝ
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Helicase, ATP-dependent.
Name=hrp; Synonyms=yadO; OrderedLocusNames=YPTB0737;
Yersinia pseudotuberculosis.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriale
Enterobacteriaceae; Yersinia.
NCBI_TaxID=633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.

STRAIN=KIM5 / Biovar Mediaevalis;

MEDLINE=22137863; PubMed=12142430;

DOI=10.1128/JB.184.16.4601-4611.2002;

Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., lerna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,

Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,

Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
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Enterobacteriaceae; Yersinia.
NCBI_TaxID=632;
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TIGR01970; DEAH box HrpB; 1.
1g; Complete proteome; Helicase; Hydrolase.
828 AA; 91983 MW; CF11FDD863330635 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OBDIA7; Q74XU2;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence upc
01-FEB-2005 (TrEMBLrel. 29, Last annotation thelicase, ATP-dependent.
Name=hrpB; OrderedLocusNames=YP0291, y0794;
Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    853 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nome sequence of Yersinia pestis KIM."; Bacteriol. 184:4601-4611(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 58.3%; 7; Conservative
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 Z., Han Y., Zhang J., .., Li M., Cui B., Qi ..
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Sodium channel alpha-subunit SCAPI.
Aplysia californica (California sea hare).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia;
Aplysioidea; Aplysiidae; Aplysia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               853;
                                                                                       91001,
Pubmed=15308053;
Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhai J., Li M., Cui B., Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang Yang H., Wang J., Huang P., Yang R.;
"Complete genome sequence of Yersinia pestis strain 91001, avirulent to humans.";
DNA Res. 11:179-197(2004).
EMBL; AE013681; AAM84381.1; -; Genomic_DNA.
EMBL; AE013128; AAS60566.1; -; Genomic_DNA.
GO; GO:0008026; F:ATP-binding; IEA.
GO; GO:0008026; F:ATP-binding; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR011545; DEAD/DEAH N.
InterPro; IPR011545; DEAH box_HrpB.
InterPro; IPR010502; Helicase_C.
InterPro; IPR001502; Helicase_C.
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DNA Cell Biol. 16:347-356(1997).
EMBL; U66915; AAC47457.1; -; mRNA.
HSSP; P04775; 1BYY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; HELICC; 1.
R01970; DEAH box HrpB; 1.
Helicase; Hydrolase.
3 AA; 95005 MW; B3DB738A18665B42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB 2; Pred. No. 2.8e+02; 1; Mismatches 2
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Pfam; PF04408; HA2; 1.
Pfam; PF00271; Helicase C; 1.
PIRSF; PIRSF005496; ATP_hel_hrpB; SMART; SM00487; DEXDC; 1.
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TISSUE=Nervous system;
MEDLINE=97238630; PubMed=9115644;
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C:membrane;
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58.3%;
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P90670 APLCA PRELIMINARY;
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Q74JK6;
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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0401D2;
13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
Hypothetical protein.
ORFNames=LmjF08.0370;
Leishmania major.
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El-Sayed N.M., Khalak
Submitted (APR-2002) t
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128 WYTLWGC 134
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STRAIN-Friedlin;
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Fremyella diplosiphon (Calothrix PCC 7601).
Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Microchaete
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Stowe-Evans E.L., Ford J., Kehoe D.M.;
Stowe-Evans E.L., Ford J., Kehoe D.M.;
"Genomic DNA Microarray Analysis: Identification of New (
Regulated by Light Color in the Cyanobacterium Fremyella
Regulated by Light Color in the Cyanobacterium Fremyella
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                                                                                                                                                                                    Ion transport; Ionic channel; Sodium channel; Sodium transfransmembrane; Transport; Voltage-gated channel.
SEQUENCE 1993 AA; 225896 MW; 33E174B9BF07E1A7 CRC64;
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ed. No. 1.2e+02;
Mismatches 1
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Stowe-Evans E., Ford J., Kehoe D.M.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ
EMBL; AY548455; AAT41947.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 168 AA; 18932 MW; 1C9DB963D521033
                                                                                                                                                                                                                                                                              Score 43.5; DB;
Pred. No. 1e+03;
3; Mismatches
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Pred. No.
InterPro; IPR002111; Cat_channel_TrpL InterPro; IPR005821; Ion_trans.
InterPro; IPR005820; M+channel_nlg.
InterPro; IPR001696; Na_channel.
InterPro; IPR010526; Na_trans_assoc.
Pfam; PF00520; Ion_trans; 4.
Pfam; PF06512; Na_trans_assoc; 1.
PRINTS; PR00170; NACHANNEL.
  channel TrpL trans.
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illarity 54.5%;
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Q6H022;
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05-JUL-2004 (TrEMBLrel. 2
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ORFNames=Tb927.5.3300;
Trypanosoma brucei.
Eukaryota; Euglenozoa;
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Q57Z63;
10-MAY-2005
10-MAY-2005
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Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannic Shallom J., Hou L., Djikeng A., Feldblyum T., Hostetler J., Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J., Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S., Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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NCBI_TaxID=5664;
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Pred. No. 1.6e+02;
1; Mismatches 1;
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Pred. No. 1.6e+02;
l; Mismatches
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Haas B., Blandin G., El-Sayed N.;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ
EMBL; AC113585; AAX79570.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 215 AA; 25574 MW; C32B79363DCDDC6
                                                                                                                                                                                         t H., Adams M.D.;
to the EMBL/GenBank/DDBJ
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Hypothetical protein.
SEQUENCE 220 AA; 26176 MW;
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137 YWLTGWSC
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NCBI TaxID=5825;
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                                                                                               E., Barretto C.,
E., Barrangou
F., Schell M.A.
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Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TaxID=237561;
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STRAIN=SC5314;
PubMed=15123810; DOI=10.1073/pnas.0401648101;
Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T
Davis R.W., Scherer S.;
"The diploid genome sequence of Candida albicans.";
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STRAIN=SC5314;

Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W., Jones T., Scherer S., Agabian N.;

"Annotation of the Genome of Candida albicans.";

Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which i
                                                                          PubMed=14983040; DOI=10.1073/pnas.0307327101;
PubMed=14983040; DOI=10.1073/pnas.0307327101;
Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C., Prittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrango Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M., "The genome sequence of the probiotic intestinal bacterium Lactobacillus johnsonii NCC 533.";
Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).

EMBL; AE017203; AAS08923.1; -; Genomic_DNA.

GO; GO:0019835; P:cytolysis; IEA.

InterPro; IPR004254; HlyIII_related.

InterPro; IPR005744; HylIII.
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB 2; Lo Pred. No. 1.6e+02; 2; Mismatches 1;
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Pred. No. 3.1e+02;
); Mismatches 2
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                                      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] STRAIN=NCC 533;
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MS; TIGR01065; hlyIII; 1.
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Local Similarity 62.5%;
nes 5; Conservative
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SEQUENCE 454 AA; 5
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ORFNames=CaO19.6606;
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GFWLLVWG 179
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059NK9;
10-MAY-2005
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NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

PubMed=15229592; DOI=10.1038/nature02579;

Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar P.

A Boisrame A., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,

A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,

A Kerrest A., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

A Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

A Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,

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               update)
                                                                         OrderedLocusNames=YALIOE204719;
Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Dipodascaceae; Yarrowia.
NCBI_TaxID=4952;
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C STRAIN=BP-1;

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S STRAIN=BP-1;

MEDLINE=22225144; PubMed=12240834;

MATANABA A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,

MATANABA C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,

Kiyokawa C., Kohara M., Takeuchi C., Yamada M., Tabata S.;

M. Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

Thermosynechococcus elongatus BP-1.";

DNA Res. 9:123-130(2002).

EMBL; BA000039; BAC08475:1; -; Genomic DNA.

GO; GO:0003824; F:catalytic activity; IEA.

InterPro; IPR001932; PP2C-1ike.

R Ffam; PF00481; PP2C; 1.

R SMART; SM0331; PP2C; 1.

S SMART; SM0331; PP2C_SIG; 1.

Complete proteome.

S SQUENCE 646 AA; 71071 MW; 56C5A74F76652D56 CRC64;
Ouail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J., Bidwell S.L., Rajandream M.A., Carucci D.J, Yates J.R., Kafatos Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S., "A comprehensive survey of the Plasmodium life cycle by genomic transcriptomic, and proteomic analyses.";

Science 307:82-86(2005).

-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; CAAJ01004254; CAH81294.1; -; Genomic_DNA.
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QBDKD6.

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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

01-MAR-2003 (TrEMBLrel. 25, Last annotation update)

7110923 protein.

OrderedLocusNames=tll0923;

Synechococcus elongatus (Thermosynechococcus elongatus).

Bacteria; Cyanobacteria; Chroococcales; Synechococcus.

NCBI_TaxID=32046;
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SUMMARIES

#### Appl 10988, A 3, Appli 15, Appl 15, Appl 6, Appl 6, Appl 6, Appl Appli Appli Appli 84, Appl 86, Appl 2, Appli 3, Appli 187, App 46926, A 9, Appli 3, Appli 8, Appli 408, App 2978, Ap 406, App 81, Appl 87, Appl o Sequence Seq equence sequence sequence sequence sequence Descripti US-09-562-737-84 US-09-107-532A-6945 US-09-107-532A-6945 US-09-354-147C-2 US-09-354-147C-3 US-09-354-147C-3 US-09-354-147C-3 US-09-354-147C-3 US-09-325-932A-187 US-09-270-767-46926 US-09-792-616-9 US-09-792-616-9 US-09-792-616-9 US-09-792-616-9 US-09-792-616-9 US-09-792-616-9 US-09-792-616-9 US-09-792-616-3 US-09-792-616-3 US-09-792-616-3 US-09-792-616-3 US-09-547-7-87 US-09-920-653B-3 US-09-920-653B-3 US-09-920-653B-3 US-09-920-653B-3 US-09-920-653B-3 US-09-920-653B-3 US-09-9457-571-15 US-09-457-571-16 US-09-457-571-16 $\mathbf{a}$ 1024 1024 1024 1765 1765 1222 2222 2222 2222 1024 1024 1024 11835 11835 11969 Length Query Match core Result No.

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Sequence 86, Application US/09562737

Patent No. 6428967

GENERAL INFORMATION:

APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708

CURRENT APPLICATION NUMBER: US/09/562,737

CURRENT FILING DATE: 2000-05-01
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Pred. No. 3.7e+02;
1; Mismatches 2
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ed. No. 1.6e+02;
Mismatches 1
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
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LOCATION: (B) LOCATION 1...492
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SEQUENCE DESCRIPTION: SEQ ID NO: 6945:
US-09-107-532A-6945
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Pred.
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ilarity 85.7%;
Conservative (
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illarity 63.6%;
Conservative
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                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                   LENGTH: 492 amino
TYPE: amino acid
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SOFTWARE: Patentin Ver. 2
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LENGTH: 1024
TYPE: PRT
ORGANISM: Artificial
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Best Local Similarity
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Best Local Similarity
7, Conserv
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Xaa's result from n's in SEQ ID NO: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Root
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H
                                                                                                   Root
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09354147C;
Sequence 3, Application US/09354147C;
Patent No. 6573067;
GENERAL INFORMATION:
APPLICANT: Dib-Hajj; Sulayman;
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Roof;
FILE REFERENCE: 44574-5004-01-US;
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT APPLICATION NUMBER: US 60/072,990
PRIOR PILING DATE: 1998-01-29
PRIOR PILING DATE: 1998-11-20
PRIOR PILING DATE: 1999-01-29
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1765;
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No. 6.2e+02;
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OTHER INFORMATION: Xaa at position 652 is Leu; Xaa
OTHER INFORMATION: or Lys. Xaa's result from n's i
                                                                                                 Sodium Channels
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Pred. No. 6.2e+02;
; Mismatches 2;
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                                       GENERAL INFORMATION:
APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Chan
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT APPLICATION NUMBER: US 60/072,990
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR FILING DATE: 1999-01-29
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2, Application US/09354147C
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                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Rattus norvegicus
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6; Conservative
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                                                            Length
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6.3e+02;
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6.3e+02;
0;
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6.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/647,140B
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: PCT/US99/06644
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                Mutations in a gene encod
Pseudoxanthoma Elasticum
                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PXE International, Inc.
APPLICANT: University of Hawaii
TITLE OF INVENTION: Mutations in a gene enc
TITLE OF INVENTION: Pseudoxanthoma Elastic
FILE REFERENCE: PXE-001
CURRENT APPLICATION NUMBER: US/09/792,616
CURRENT FILING DATE: 2001-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42;
Pred. No.
                                                                Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09647140B; Patent No. 6803184; GENERAL INFORMATION:
APPLICANT: Fox Chase Cancer Center; APPLICANT: Kruh, Gary D.
APPLICANT: Lee, Kun.
APPLICANT: Belinsky, Martin G.
APPLICANT: Bain, Lisa J.
TITLE OF INVENTION: Nucleic Acids and FILE REFERENCE: FCCC 98-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
                                                                                                                                                                                                                                              3, Application US/09792616
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-792-616-9
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SOFTWARE: Patentin ver
                                                                             Similarity
5; Conserv
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GYWLSLW
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SEQ ID NO 8
LENGTH: 1503
TYPE: PRT
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Best Local S
Matches 5
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Best Local S
Matches 5
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Best Local
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US-09-792-616-9
Sequence 9, Application US/09792616
Sequence 9, Application US/09792616
Sequence 9, Application US/09792616
Sequence 9, Application US/09792616
GENERAL INFORMATION:
TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRF TITLE OF INVENTION: Pseudoxanthoma Elasticum
FILE REFERENCE: PXE-001
CURRENT APPLICATION NUMBER: US/09/792,616
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 1498
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
          RESULT 6

US-09-325-932A-187

US-09-325-932A-187

Sequence 187, Application US/09325932A

Patent No. 6451604

GENERAL INFORMATION:

APPLICANT: Flinn, Barry

APPLICANT: Lasham, Annette

TITLE OF INVENTION: Compositions affecting programmed cell

TITLE OF INVENTION: death and their use in the modification of f

TITLE OF INVENTION: death and their use in the modification of f

TITLE OF INVENTION: death and their use in the modification of f

CURRENT APPLICATION NUMBER: US/09/325,932A

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 206

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 187

LENGTH: 161
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US_09-270-767-46926

Sequence 46926, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic acids and proteins of Droty FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 46926

LENGTH: 273
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Pred. No. 1.2e+02;
; Mismatches 1;
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Pred. No. 7
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Conservative
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ilarity 75.0%;
Conservative
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6; Conserv
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Matches 6
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US-09-2
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US-09-3
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US-09-134-000C-3630
; Sequence 3630, Application US/09134000C
; Sequence 3630, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
    TITLE OF INVENTION:
    TITLE OF INVENTION: BUTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032.
    CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTHARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; I
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ed. No. 1.5e+02;
Mismatches 1
                                                                                                                                                           APPLICATION NUMBER: US 09/071,035
FILING DATE: 1998-05-04
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PB369P1D1
                                       COMPUTER: Dell Latitude
COMPUTER: Dell Latitude
COBERATING SYSTEM: Windows 98
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/206,576
FILING DATE: 29-Jul-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                    NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acid
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US-09-134-000C-3630
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62.5%;
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62.5%;
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ZIP: 20850
COMPUTER READABLE FORM:
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                             MEDIUM TYPE:
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GTWITLWG
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Matches 5; Conser
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SEQUENCE
US-10-206-576-408
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LENGTH: 229
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                                                                                                                 US-09-071-035-408

US-09-071-035-408

Sequence 408, Application US/09071035

GENERAL INFORMATION:

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 496

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA
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TITLE OF INVENTION: Enterococcus faecalis Polynucleotides
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
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Indels
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STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
Mismatches
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Pred. No. 1
                                                                                                                                                                                                                                                                                             ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII TAVE
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Patent No. 6913907
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 408:
SEQUENCE CHARACTERISTICS:
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62.5%; Pri
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amino acid
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CURRENT APPLICATION DATA
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 Conservative
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APPLICATION NUMBER:
FILING DATE:
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FILING DATE:
CLASSIFICATION:
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Search completed: May 3
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                                                                 APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2978
LENGTH: 264
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Mismatches
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Pred. No.
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Pred. No.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 406:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 406, Application US/09071035; Sequence 406, Application US/09071035; Patent No. 6448043; GENERAL INFORMATION:
TITLE OF INVENTION: Enterococcus fate NUMBER OF SEQUENCES: 496; CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: Human Genome Sciences, STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
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Avenue
 US-09-540-236-2978
; Sequence 2978, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
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; ORGANISM: M.catarrhalis
US-09-540-236-2978
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US-09-071-035-406
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ZIP: 208
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278, App
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77862, A
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US-10-292-798-1934

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US-10-981-738-36

US-10-981-738-46

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US-10-981-738-56 US-10-981-738-58 US-10-981-738-60	-10-981-738-6 -10-981-738-6 -10-981-738-6	10-981-738-70 10-981-738-72 10-767-701-54 10-981-738-13	-10-462-262-297 -10-369-493-19313 -10-032-585-7816 -10-437-963-16019	82-122A- 37-963-1
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Sequence 34, Application US/10046922;
Publication No. US20020164667A1;
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS;
FILE REFERENCE: 28967/37084A;
CURRENT APPLICATION NUMBER: US/10/046,922;
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 34
LENGTH: 10
Sequence 35, Application US/10046922
Sequence 35, Application US/10046922
Publication No. US20020164667A1
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 28967/37084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
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10; Conservative
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             LOCATION: (73)
OTHER INFORMATION: Variable amino acid
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US-10-046-922-73

Sequence 73, Application US/10046922

Publication No. US20020164667A1

GENERAL INFORMATION:

APPLICANT: Alitalo, Kari

APPLICANT: Kubo, Hajime

TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS

FILE REFERENCE: 28967/37084A

CURRENT APPLICATION NUMBER: US/10/046,922

CURRENT FILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 80

SOFTWARE: PatentIn version 3.0
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US-10-017-161-2288

Sequence 2288, Application US/10017161

Publication No. US20030143668A1

GENERAL INFORMATION:

APPLICANT: ASAI, KIYOSHI

APPLICANT: ASAI, KIYOSHI

APPLICANT: ABURATANI, HIROYUKI

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 084335/0152

CURRENT APPLICATION NUMBER: US/10/017,161

CURRENT APPLICATION NUMBER: JP 2001/246789

PRIOR APPLICATION NUMBER: JP 2001/246789

PRIOR FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2430

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2288

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CTHER INFORMATION: X i.

NAME/KEY: SITE

LOCATION: (9)..(9)

CTHER INFORMATION: X i.

US-10-046-922-73
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OTHER INFORMATION: X NAME/KEY: SITE LOCATION: (10)..(10) OTHER INFORMATION: X
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   ; OTHER INFORMA; LOCATION: (10; OTHER INFORMAUS-10-046-922-34
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LENGTH: 10
TYPE: PRT
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Best Local S
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; LOCATION: (256)..(289)
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APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASURATANI, HIROYUKI
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COU
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1934
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LOCATION: (219)..(219)
OTHER INFORMATION: Variable amino acid
FEATURE:
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3-10-292-798-1934
Sequence 1934, Application US/10292798
Publication No. US20030235833A1
GENERAL INFORMATION:
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OTHER INFORMATION: Variable
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LOCATION: (107)..(107)
OTHER INFORMATION: Variable
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ORGANISM: Homo sapiens
FEATURE:
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LOCATION: (121)..(121)
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LOCATION: (178)..(178)
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LOCATION: (73)..(73)
OTHER INFORMATION: Va
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LOCATION: (80)..(83)
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APPLICANT: Billutla, Renuka C.
APPLICANT: Billutla, Renee
APPLICANT: Brissette, Renee
APPLICANT: Brissette, Renee
APPLICANT: Brissette, Michael
APPLICANT: Dedova, Olga
APPLICANT: Dedova, Olga
APPLICANT: Dedova, Olga
APPLICANT: Dedova, Olga
APPLICANT: Goldstein, Neil I.
APPLICANT: Goldstein, Noil I.
APPLICANT: Goldstein, Noil I.
APPLICANT: Goldstein, Noil I.
AURRENT APPLICATION NUMBER: US/10/280, 066
CURRENT APPLICATION NUMBER: Go/345,471
PRIOR APPLICATION NUMBER: 60/345,471
SPRIOR FILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 537
SOFTWARE: PatentIn version 3.1
SEQ ID NO 476
LENGTH: 25
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Sequence 125253, Application US/10437963

Sequence 125253, Application US/10437963

Sequence 125253, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B

FILE REFERENCE: 38-21(53221)B
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                                                                                                                 Mismatches
                                                                47.5;
No. 1
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CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 125253
LENGTH: 63
amino acid
                                                                    Score
Pred.
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; Sequence 476, Application US/10280066
; Publication No. US20030180718A1
; GENERAL INFORMATION:
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; OTHER INFORMATION: Tiel-20C-3-D116
US-10-280-066-476
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illarity 60.0%;
Conservative
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Best Local Similarity 66.7%;
Matches 6; Conservative
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FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: (1)...(136)
; OTHER INFORMATION: Xaa = any a
; OTHER INFORMATION: in Example
US-10-112-944-743
                         63.9%;
ilarity 66.7%;
Conservative
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APPLICATION NUMBER: US C
FILING DATE: 2000-03-07
APPLICATION NUMBER: US C
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Wang, Dunrui
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an, Tom
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Weng, Gezhi
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Zhiwei
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                                       Similarity.
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Best Local Similarity
Matches 6; Conser
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CGFWPRIWG
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Wehrman,
                                                                              CGYWLTIWG
                                                                                                                                                                                   Publication No. US20
GENERAL INFORMATION:
APPLICANT: Tang, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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US-10-282-122A-77862
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FILE REFERENCE:
US-10-462-262-278
                         Query Match
Best Local S
Matches 6
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                      APPLICANT: Rondon, Isaac Jesus
APPLICANT: Rondon, Isaac Jesus
APPLICANT: Wu, Qi-Long
APPLICANT: Ley, Arthur C.
APPLICANT: Stochl, Mark
APPLICANT: Ransohoff, Thomas C.
APPLICANT: Ransohoff, Thomas C.
APPLICANT: Potter, M. Daniel (deceased)
TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 3421.1006-001
CURRENT APPLICATION NUMBER: US/10/125,869A
CURRENT FILING DATE: 2002-11-19
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 200
SOFTWARE: FastSEQ for Windows Version 4.0
                                           PAT_MRT4530_27915C.1.pep
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15;
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Mismatches
                                                                                 Score 47; DB Pred. No. 33;
                                                                                                d. No. 33;
Mismatches
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Sequence 278, Application US/10462262

Publication No. US20040009534A1

GENERAL INFORMATION:

APPLICANT: Sato, Aaron K.

APPLICANT: Dawson, Bruce M.

TITLE OF INVENTION: PROTEIN ANALYSIS

FILE REFERENCE: 10280-052001

CURRENT APPLICATION NUMBER: US/10/462,262

CURRENT FILING DATE: 2003-06-16

PRIOR FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 430

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46;
Pred. No.
                                                                                                                                                                                                                                 Sequence 54, Application US/10125869A Publication No. US20030199671A1 GENERAL INFORMATION:
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ilarity 66.7%;
Conservative
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ORGANISM: Artificial Sequence
                                           Clone ID:
                                                                               Similarity 60.0%; 6; Conservative
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                sativa
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US-10-125-869A-54
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                                                                                                                                                     37 CGHYLKAWGC
                                                                                                                                      CGYWLTIWGC
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ORGANISM: Oryza sati
FEATURE:
OTHER INFORMATION: C
S-10-437-963-125253
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ENGTH: 17
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LENGTH: 17
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Best Local S
Matches 6
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OTHER IN
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Length 17;
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                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Zhiwei
TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids
TITLE OF INVENTION: Secreted Polypeptides
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Score 46; DB
Pred. No. 15;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/112,944
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/491,404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-03-07
NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 09/491,404
FILING DATE: 2000-01-25
APPLICATION NUMBER: US 09/496,914
FILING DATE: 2000-02-03
APPLICATION NUMBER: US 09/515,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 09/552,929
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2000-03-31
                                                                                                                                                                          Application US/10112944 . US20040048249A1
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PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 924
SOFTWARE: pt_FL_genes Version 5
SEQ ID NO 743
LENGTH: 136
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CURRENT APPLICATION NUMBER: US/10/981,738
CURRENT FILING DATE: 2004-11-05
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                .50, Application US/10437963
                                                                                                                       Score Pred.
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У
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Sequence
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ilarity 50.0%;
Conservative
                               Sequence
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                                                                                                                        61.8%;
54.5%;
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892 CGHWIETMWDC
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             TYPE: PRT
ORGANISM: Artificial
FEATURE:
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; Sequence 181150, Appli
; Publication No. US2004
; GENERAL INFORMATION:
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Best Local Similarity
Matches 4; Conser
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WWVSVWGC
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Best Local Similarity
Matches 6; Conser
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CTHER INFORMATION:
US-10-211-962-84
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US-10-211-962-84

Sequence 84, Application US/10211962

Publication No. US20030082640A1

GENERAL INFORMATION:

APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708

CURRENT APPLICATION NUMBER: US/10/211,962

CURRENT FILING DATE: 2002-08-01

PRIOR FILING DATE: 2000-05-01

NUMBER OF SEQ ID NOS: 132

SOFTWARE: PatentIn Ver: 2.1
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5e+02;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prior Application data removed
     Application US/10282122A
US20040029129A1
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3ER: 60/191,078
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H
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APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Forsyth, R.
APPLICANT: Yamamoto, Robert
APPLICANT: You, H.
TITLE OF INVENTION: Identificati
FILE REFERENCE: ELITRA.034A
CURRENT FILING DATE: 2003-02-26
PRIOR APPLICATION NUMBER: 60/206
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-06
PRIOR APPLICATION NUMBER: 60/230
                                                                                                                                                                                                                                                                                                                                                                                                                                                   R FILING DATE: 2000-09-09
R APPLICATION NUMBER: 60/24
R FILING DATE: 2000-10-23
R APPLICATION NUMBER: 60/25
R FILING DATE: 2000-11-27
R APPLICATION NUMBER: 60/25
R FILING DATE: 2000-12-22
R FILING DATE: 2000-12-22
R FILING DATE: 2000-12-22
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58.3%;
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Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
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                                                      Rang, Liangsu
Zamudio, Carlos
Malone, Cheryl
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7; Conserv
         Sequence 77862, App. Publication No. US26 GENERAL INFORMATION
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APPLICANT: Bruenker, Peter
APPLICANT: Suter, Tobias
APPLICANT: Puentener, Ursula
APPLICANT: Puentener, Ekkehard
APPLICANT: Ferrara, Claudia
TITLE OF INVENTION: Affinity and Effector Function
FILE REFERENCE: 1975.0290001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; L.1.3e+02;
                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Xovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and
TITLE OF INVENTION: Plants and Uses Thereof for Pl
FILE REFERENCE: 38-21(53221)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 181150
LENGTH: 103
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                                                            ore 44.5; DB 4 ed. No. 7e+02; Mismatches
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RESULT 15
US-10-981-738-30
; Sequence 30, Application US/10981738
; Publication No. US20050123546A1
; GENERAL INFORMATION:
   APPLICANT: Umana, Pablo
; APPLICANT: Bruenker, Peter
; APPLICANT: Bruenker, Peter
; APPLICANT: Bruenker, Draula
; APPLICANT: Bruenker, Draula
; APPLICANT: Bruenker, Draula
; APPLICANT: Puentener, Ursula
; APPLICANT: Puentener, Ursula
; APPLICANT: Moessner, Ekkehard
; APPLICANT: Moessner, Claudia
; TITLE OF INVENTION: Affinity and Effector Function
; FILE REFERENCE: 1975.0290001
; CURRENT APPLICATION NUMBER: US/10/981,738
; CURRENT APPLICATION NUMBER: US/10/981,738
; CURRENT PILING DATE: 2004-11-05
; VUMBER OF SEQ ID NOS: 78
; SEQ ID NO 30
; LENGTH: 119
; TYPE: PRT
; CORGANISM: Artificial
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Pred. No. 1.4e+02;
0; Mismatches 2; Indels
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; OTHER INFORMATION: Mouse-human chimeric polypeptide
US-10-981-738-30
                                                                                      Score 44; DB 5; Le
Pred. No. 1.3e+02;
0; Mismatches 2;
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Matches 6; Conservative
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; TYPE: PRT
; ORGANISM: Mu
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(SIDSS/ptodata/2/pubpaa/US07 NEW PUB.pep:*

(SIDSS/ptodata/2/pubpaa/PCT NEW PUB.pep:*

(SIDSS/ptodata/2/pubpaa/US09 NEW PUB.pep:*

(SIDSS/ptodata/2/pubpaa/US09 NEW PUB.pep:*

(SIDSS/ptodata/2/pubpaa/US10 NEW PUB.pep:*

(SIDSS/ptodata/2/pubpaa/US11 NEW PUB.pep:*
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Biocceleration Ltd
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US-11-264-096-1534

US-11-087-099-2305

US-10-995-561-968

US-11-124-367A-322

US-11-124-367A-321

US-11-124-367A-321

US-11-124-367A-321

US-11-124-367A-321

US-11-124-367A-321

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US-11-124-367A-321

US-11-124-367-19834

US-11-250-411-97

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US-11-087-099-983

US-11-087-099-6672
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US-11-264-096-1534
; Sequence 1534, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
US-11-264-U96-1533, Application US/11264096 Sequence 1533, Application US/11264096 Publication No. US20060084794A1 GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Albumin Fusion Proteins FILE REFERENCE: PF546D1 CURRENT APPLICATION NUMBER: US/11/264,096 CURRENT FILING DATE: 2005-11-02 PRIOR APPLICATION NUMBER: 60/229, 358 PRIOR FILING DATE: 2000-04-12 PRIOR FILING DATE: 2000-12-21 PRIOR APPLICATION NUMBER: 60/256, 931 PRIOR FILING DATE: 2000-12-21 PRIOR FILING DATE: 2000-12-21 PRIOR FILING DATE: 2000-04-25 NUMBER OF SEQ ID NOS: 2267 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1533 LENGTH: 152
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Pred. No. 22;
1; Mismatches
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illarity 70.0%;
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; Sequence 968, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, MET
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT FILING DATE: 2004-11-24
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: Genes and Uses for Plant Erent Bence: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 2305
LENGTH: 441
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Pred. No.
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CURRENT FILING DATE: 2005-11-02
PRIOR APPLICATION NUMBER: 09/833,245
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1534
LENGTH: 159
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2305, Application US/11087099 Publication No. US20060041961A1 GENERAL INFORMATION:
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; ORGANISM: Sinorhizobium meliloti
US-11-087-099-2305
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illarity 70.0%;
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ilarity 71.4%;
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US-11-264-096-1534
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LENGTH: 1023
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                                                                                                                                                                                                        TYPE: PRT ORGANISM:
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                                                                                                                                                                                                                                                                                                 US-11-124-367A-322

Sequence 322, Application US/11124367A

Publication No. US20060024700A1

GENERAL INFORMATION:

APPLICANT: Michele Cargill
APPLICANT: Michele Cargill
APPLICANT: Hongjin Huang

TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses T
FILE REFERENCE: CLO0159.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A

CURRENT FILING DATE: 2005-05-09

PRIOR APPLICATION NUMBER: US 60/568,846

PRIOR FILING DATE: 2004-06-05

PRIOR FILING DATE: 2004-06-05

PRIOR FILING DATE: 2004-06-05

NUMBER OF SEQ ID NOS: 34460

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 322

LENGTH: 395
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Pred. No. 71;
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Mismatches
Pred. No. 91;
2; Mismatches
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Pred. No.
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US-10-374-954-2
; Sequence 2, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR ST
; TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL,
; FILE REFERENCE: 1242/41/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Vanderbilt University
APPLICANT: George, Alfred L
APPLICANT: George, Alfred L
APPLICANT: Lossin, Christoph
TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR S'
TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL,
FILE REFERENCE: 1242/41/2
CURRENT APPLICATION NUMBER: US/10/374,954
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: US 60/359,382
PRIOR FILING DATE: 2002-02-25
                                           APPLICANT: Vanderbilt University
APPLICANT: George, Alfred L
APPLICANT: George, Alfred L
APPLICANT: Lossin, Christoph
TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR S'
TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL,
FILE REFERENCE: 1242/41/2
CURRENT APPLICATION NUMBER: US/10/374,954
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: US 60/359,382
PRIOR FILING DATE: 2002-02-25
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Pred. No. 2.3e+02;
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Mismatches
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Pred. No. 2
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lication US/10374954
US20050260576A1
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illarity 54.5%;
Conservative
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SOFTWARE: Patentin ver
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SOFTWARE: Patentin ver
SEQ ID NO 23
LENGTH: 1981
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  Sequence 23, Applica Publication No. US2 GENERAL INFORMATION
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LENGTH: 1998
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; ORGANISM: HO
US-10-374-954-21
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Best Local S
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
LENGTH: 268
TYPE: nor
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                                                                                                               Sequence 321, Application US/11124367A

Publication No. US20060024700A1

GENERAL INFORMATION:

APPLICANT: Michele Cargill

APPLICANT: Hongjin Huang

TITLE OF INVENTION: Genetic Polymorphisms Associated with

TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof

FILE REFERENCE: CLOO1519.ORD

CURRENT APPLICATION NUMBER: US/11/124,367A

CURRENT APPLICATION NUMBER: US 60/568,846

PRIOR FILING DATE: 2004-05-07

PRIOR FILING DATE: 2004-06-25

PRIOR FILING DATE: 2004-06-25

PRIOR FILING DATE: 2004-06-25

PRIOR FILING DATE: 2004-06-25

PRIOR FILING DATE: 2004-08-09

NUMBER OF SEQ ID NOS: 34460

SOFTWARE: FastSEQ for Windows Version 4.0
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Mismatches
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; Sequence 19834, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al
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ilarity 55.6%;
Conservative (
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54.5%;
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LOCATION: (1)...(268)
OTHER INFORMATION: Cere
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                                        GIWFLFWGC
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US-11-124-367A-321
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US-10-374-954-23
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Best Local S
Matches 6
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Sequence 101, Appropries Publication No.
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PRIOR FILING I PRIOR APPLICATION PRIOR FILING I NUMBER OF SEQ SOFTWARE: Pattern SEQ ID NO 97
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US-11-250-411-86
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LENGTH: 119
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US-11-2
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APPLICANT: CHAN, KWOK HUNG

APPLICANT: CHAN, KWOK HUNG

APPLICANT: CHAN, KWOK HUNG

APPLICANT: PEIRIS, JOSEPH S.M.

APPLICANT: PEIRIS, JOSEPH S.M.

TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT

TITLE OF INVENTION: INFECTION AND USES THEREOF

FILE REFERENCE: V0690.0044

CURRENT APPLICATION NUMBER: US/11/129,741

CURRENT FILING DATE: 2005-05-16

PRIOR APPLICATION NUMBER: 10/895,064

PRIOR FILING DATE: 2004-07-21

NUMBER OF SEQ ID NOS: 4257

SOFTWARE: PATENTIN VERSION 3.3

SEQ ID NO 3641

LENGTH: 10
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Sequence 97, Application US/11250411

Publication No. US20060034838A1

GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KAWADA, YOKO
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: SHIBUYA, MASABUMI
TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANT
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                                                                                                                                                                                                  Length 2009;
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                                                                                                                                                                                                   Score 40.5;
Pred. No. 2.
CURRENT APPLICATION NUMBER: US/10/374,954
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: US 60/359,382
PRIOR FILING DATE: 2002-02-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 249-107
CURRENT APPLICATION NUMBER: US/11/250,411
CURRENT FILING DATE: 2005-10-17
PRIOR APPLICATION NUMBER: US/09/453,718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3641, Application US/11129741 Publication No. US20060034853A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TT: YUEN, KWOK YUNG
TT: WOO, CHIU YAT PATRICK
TT: LAU, KAR PUI SUSANNA
TT: CHAN, KWOK HUNG
TT: POON, LIT MAN
TT: PEIRIS, JOSEPH S.M.
TT: GUAN, YI
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larity 54.5%;
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GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: KAWADA, YOKO
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: SHIBUYA, MASABUMI
ITILE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
FILE REFERENCE: 249-107
CURRENT APPLICATION NUMBER: US/11/250,411
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: US/09/453,718
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1991-11-21
                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-11-250-411-97
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DR FILING DATE: 1999-12-03
DR APPLICATION NUMBER: 09/315,051
DR FILING DATE: 1999-05-20
DR APPLICATION NUMBER: 09/119,014
DR FILING DATE: 1998-07-20
DR APPLICATION NUMBER: PCT/JP97/04259
DR FILING DATE: 1997-11-21
SER OF SEQ ID NOS: 111
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Pred. No.
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Pred.
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ORGANISM: Artificial
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Best Local Similarity
- Local 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial
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APPLICANT: SHITARA, KENYA
APPLICANT: TTO, MIKITO
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: KAWADA, YOU
APPLICANT: KAWADA, YOU
APPLICANT: KAWADA, YOU
APPLICANT: KAWADA, WASABUMI
TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBOD
FILE REPERBNCE: 249-10-17
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: US/09/453,718
PRIOR APPLICATION NUMBER: US/09/453,718
PRIOR APPLICATION NUMBER: US/09/15,051
PRIOR PILING DATE: 1999-05-20
PRIOR PILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: PCT/JP97/04259
PRIOR PILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIN Ver: 2.1
SOFTWARE: PATENTING DATE: 1998-07-20
TYPE: PRT
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: Synthetic pro
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Indels

3;

138;

Length

11;

Score 40; DB 1 Pred. No. 46; 0; Mismatches

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Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative

2, 2006, 09:33:44

Search completed: May Job time: 14.186 secs

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122 GYWFAYWG

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Biocceleration Ltd
version - 2006
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         Copyright
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es/sec Search time 78.9535 Seconds (without alignments) 38.955 Million cell update

US-10-046-922-67 35 score: Title

7 GYWXXXW Perfect so Sequence:

Gapext BLOSUM62 Gapop 10.0 Scoring table:

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2443163 segs, 439378781 Searched 2443163 hits satisfying chosen parameters: of Total number

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Database

Geneseq\_21:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description		Desired National	99769 Rhesus D	03644 Group B	Protein	44861 Bacter	38334 Protein	Abu24881 Protein	30560 Streptoc	10245 Protein	Protei	24700 Bacteria	7906 Streptoc	31356 Strepto	v79159 Strep	C97241 E.	968 St	55389 Lac	55385 La	74582 Pseud	u22414 Protein	49403 M	o24081 Epigene	583 HIV-	
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## ALIGNMENTS

antibody binding peptide SEQ ID NO:4 Z AAB99759 standard; peptide; 10 (first entry) 21-SEP-2001 Д AAB99759 Rhesus RESULT 1 AAB99759 

Rhesus D antibody binding peptide, Rhesus D; RhD; identification; anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy; prophylaxis; haemolytic disease of the newborn; HDN; ITP; idiopathic thrombocytopaenic purpura; immunoglobulin.

Homo sapiens

EP1106625-A1.

13-JUN-2001.

17-NOV-1999;

99EP-00122858. 17-NOV-1999;

(ZLBB-) ZLB BIOPLASMA

Fisch Hofmann A, s, Miescher

2001-383568/41. WPI;

the of Novel peptides capable of binding Rhesus D antibodies are used to manufacture an agent for the diagnosis, therapy or prophylaxis of diseases associated with Rhesus D antigen, e.g. hemolytic disease newborn (HDN).

Page 12; 19pp; English. 1; Claim

The present sequence represents a peptide capable of binding Rhesus D antibodies (I). Also described in the present invention are: (1) a nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more (II) operably linked to an expression control system; (3) a cell (IV) comprising (II) or (III); (4) preparing (I); (5) identifying (M1) peptides having immunologic properties of Rhesus D protein epitopes comprising subjecting an antibody/antibody fragment recognising an epitope of Rhesus D protein to several panning rounds with a phage display library, and identifying immunogenic peptide sequences which are

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of the
mimotopes which differ in their amino acid sequence from the amino acid sequences of Rhesus D protein; and (6) peptides (V) with immunological properties of Rhesus D protein epitopes obtained by (M1). (I) is used to manufacture an agent for the diagnosis, therapy or prophylaxis of diseases associated with Rhesus D antigen, e.g. haemolytic disease of the newborn (HDN) or idiopathic thrombocytopaenic purpura (ITP), for the manufacture of an affinity reagent for anti-Rhesus D antibodies purified or removed from body fluids or immunoglobulin preparations. Using (I) as an immunogen to raise anti-Rhesus D antibodies avoids using immunisation with foreign erythrocytes thereby avoiding the risk of transmission of viral diseases like AIDS and hepatitis B
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Sequence 10 AA;

ö Indels Length ., M 4 ; DB d. No. 12; Mismatches Score 34; Pred. No. ö 97.1%; ilarity 57.1%; Conservative 7 7 Similarity GYWSAKW GYWXXXW 4 Query Match Best Local Matches Best В ð

RESULT

standard; peptide; AAB99769 AAB99769

(first 21-SEP-2001 AAB99769;

antibody related peptide Rhesus D

#2

entry)

ö peptide; Rhesus D; RhD; identification; Rhesus D antibody binding peptide; Rhesus D; RhD; identificatio anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy; prophylaxis; haemolytic disease of the newborn; HDN; ITP; cycliidiopathic thrombocytopaenic purpura; immunoglobulin; circular.

Homo sapiens Synthetic.

Location/Qualifiers 1. .12 Disulfide-bond

EP1106625-A1

13-JUN-2001

99EP-00122858 17-NOV-1999 99EP-00122858 17-NOV-1999;

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Н Fisch Hofmann A, 2001-383568/41 ŝ Miescher

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peptides capable of acture an agent for ses associated with

manufacture an

Novel

diseases

1; Page 8; 19pp; English. Example

(HDN)

newborn

more one or (1) ieus D The present invention describes peptides capable of binding Rhesus I antibodies (I). Also described in the present invention are: (1) a nucleic acid (II) encoding (I); (2) a vector (III) comprising one on (II) operably linked to an expression control system; (3) a cell (I/ comprising (II) or (III); (4) preparing (I); (5) identifying (M1) peptides having immunologic properties of Rhesus D protein epitopes comprising subjecting an antibody/antibody fragment recognising an epitope of Rhesus D protein to several panning rounds with a phage 

display library, and identifying immunogenic peptide sequences which are mimotopes which differ in their amino acid sequence from the amino acid sequences of Rhesus D protein; and (6) peptides (V) with immunological properties of Rhesus D protein epitopes obtained by (M1). (I) is used to manufacture an agent for the diagnosis, therapy or prophylaxis of diseases associated with Rhesus D antigen, e.g. haemolytic disease of the newborn (HDN) or idiopathic thrombocytopaenic purpura (ITP), for the manufacture of an affinity reagent for anti-Rhesus D antibodies purified or removed from body fluids or immunoglobulin preparations. Using (I) as an immunogen to raise anti-Rhesus D antibodies avoids using immunisation with foreign erythrocytes thereby avoiding the risk of transmission of viral diseases like AIDS and hepatitis B. The present sequence represents an anti-Rhesus D (RhD) antibody related peptide which is used in an anti-Rhesus D (RhD) antibody related peptide which is used in an 

Sequence 12 AA;

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Gaps

ô Gaps .; 0 Length 12; Indels ж ; 4 , Mismatches DB Score 34; Pred. No. ö 97.1%; larity 57.1%; Conservative Similarity 4; Query Match Best Local Matches

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protein; 452 AA AAU03644 standard; AAU03644 RESULT

AAU03644;

(first entry) 12-SEP-2001

ID-119 antigenic protein, Streptococcus m Group

sepsis; tract; Group B Streptococcus; encapsulated bacterium; therapeutic; meningitis; neonate; antigenic; vaccine; infection; genital capsid polysaccharide vaccination.

Streptococcus agalactiae

WO200132882-A2

10-MAY-2001

2000WO-GB003437 07-SEP-2000; 07-SEP-1999;

(MICR-) MICROBIAL TECHNICS LTD

SB; Hanniffy Wells JM, RWF, Page Le

WPI; 2001-316444/33. N-PSDB; AAS07061. 

New polypeptides derived from Streptococcus agalactiae are useful to provide detection of, and vaccination against, Group B Streptococcus infections, particularly to prevent infection in neonatals. 

Claim 1; Fig 1; '178pp; English

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86 to of

binding Rhesus D antibodies are used the diagnosis, therapy or prophylaxis Rhesus D antigen, e.g. hemolytic diseas

AAU03601-AAU03722 represent Group, B Streptococcus (Streptococcus agalactiae is an encapsulated bacterium which is a major pathogen of humans causing sepsis and meningitis in neonates as well as adults. The S. agalactiae antigenic polypeptides are used to vaccinate against Group B Streptococcus infections, particularly to prevent infection in new born children arising from the maternal genital tract. An immunogenic composition is useful in the preparation of a medicament for the treatment or prophylaxis of Group B Streptococcus infection. The invention does not have the disadvantages of varied response rate associated with prior art

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid concaining a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host.cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding antisense nucleic acid; (4) an antibody capable of specifically binding che polypeptide; (6) inhibiting cellular the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway. It which a proliferation or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which the test compound that inhibits proliferation of an or agene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the extent product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of
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Forsyth |
                                                          Length
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                                                     DB 4; LC.
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   Group
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Yamamoto R,
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                                                          ore 34; DB ed. No. 4.4e Mismatches
capsid polysaccharide vaccination against
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                                                             Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                essential
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2001US-00948993.
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                                                                                                                                                                                                                              standard; protein;
                                                         Similarity 57.1%;
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                  Antisense; prokaryotic
                                                                                                                                                                                                                                                                                                                                                                               Burkholderia fungorum.
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ξυ,
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N-PSDB; ACA25459.
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06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
06-MAR-2002;
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                                   452
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                                    Sequence
                                                                Query Match
Best Local
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ABU21589
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strains, or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a recombinant DNA construct comprising a promoter is positioned t promoter functional in a plant cell, where the promoter is positioned t provide for expression of a polynucleotide encoding a polypeptide from microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant is a crop plant ransformed plant is a crop plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A construct comprising a promoter positioned to provia polynucleotide encoding a polypeptide from a useful for producing plants with improved properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carbohydrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             kecombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
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Pred. No. 4.5e+02;
); Mismatches 3;
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                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                        standard; protein;
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4; Conservative
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HINKLE
SLATER
CHEN X.
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Best Local S
Matches 4
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ADS44861
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cuch as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties.

The recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.html.
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Xu HH;
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Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein encoded by Prokaryotic essential gene #23861
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Pred. No. 4.6e+02;
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Yamamoto R,
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2001US-00948993.
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2002US-0362699P.
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57.1%;
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B; ACA42204.
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Trawick
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06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
06-MAR-2002;
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N-PSDB;
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Wall
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

66258; 1766pp; English

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Claim

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cuncing a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding cantisense nucleic acid; (4) an antibody capable of specifically binding collideration or the activity of agene in an operon required for proliferation or the activity of a gene in an operon required for the gene product or that has an activity aginst a biological pathway required for proliferation, or that inhibites cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or owhich each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the trarget prokaryotic essential genes a Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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Xu HH;
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Forsyth
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Mismatches
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Yamamoto R,
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Pred. No.
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2001US-00948993.
2001US-0342923P.
2002US-00072851.
2002US-0362699P.
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ilarity 57.1%;
Conservative
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Best Local Similarity
4, Conserv
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N-PSDB; ACA28751.
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Trawick
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25-OCT-2001;
08-FEB-2002;
06-MAR-2002;
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ABU24881
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide; (2) producing the polypeptide; (3) an isolated by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of agene in an operon required for proliferation, or that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation; (8) identifying a gene required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiolic; (10) profilling a compound; a activity; (11) a culture comprising strains in which the strains or (13) identifying the target of a compound that inhibits the strains; or (13) identifying the target of a compound that inhibits the carains or (13) identifying the target of a compound that inhibits the carains or (13) identifying for homologous nucleic acids are useful for for cellular proliferation to isolate candidate molecules for rational contents or cellular proliferation or for enreaning for homologous nucleic acids required for a compound collection of an organism. The antisense molecules for rational collection of an organism or for enreaning for homologous nucleic acids required for a content or cellular proliferation or for enreaning for homologous nucleic acids required for the processing the foreign and the processing or for enreaning for for enreaning for production or cellular proliferation or for enreaning for enreaning for acids are useful for the product is over the process or collection or cellu
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                New antisense nucleic acids, useful for identifying proteins or scretor homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              drug discovery programs, or for screening homologous nucleic at required for proliferation in cells other than S. aureus, S. t) K. pneumoniae or P. aeruginosa. The present sequence is encoded that arget prokaryotic essential genes. Note: The sequence date patent did not form part of the printed specification, but was in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 474;
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Pred. No. 4.6e+02;
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                                                                                                          SEQ ID NO 52805; 1766pp; English
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57.1%;
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. (I) A composition comprising (I) or a nucleic acid encoding (I), may be biological sample. (I) is used to determine whether a compound binds to biological sample. (I) is used to determine whether a compound binds to used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                  or
                                                                                                                                                                             infection, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     design
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                                                                                                                                                                               New Streptococcus protein for the treatment or prevention of disease caused by Streptococcus bacteria, such as meningitis, detecting a compound that binds to the protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 475;
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Pred. No. 4.6e+02;
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2001US-00948993.
2001US-0342923P.
2002US-00072851.
2002US-0362699P.
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24-NOV-2000; 2000GB-00028727
07-MAR-2001; 2001GB-00005640
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GENOMIC
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N-PSDB; ABN71191.
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Best Local Similarity
Matches 4; Conser
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06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
06-MAR-2002;
                                                                                                                                                                                                                                                   Claim 1; Page
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The invention relates to an isolated nucleic acid comprising any one of the nucleic acid inhibits proliferation of a cell. Also included are of the nucleic acid inhibits proliferation of a cell. Also included are coff the nucleic acid inhibits proliferation of a cell. Also included are encoding a polypeptide whose expression is inhibited by the antisense concleic acid; (4) an exter concern; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense concleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular concernse proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway concerns for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product is organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying an expension. The antisense nucleic acids are useful for proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for proliferation in cislate candidate molecules for retional crudical provers or collection in cells other than S. aureus, S. typhimurium, T. P. Parger
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for this
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                                       nd JW;
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                                       Zyski
Xu HH
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                                                                                                                                                       New antisense nucleic acids, useful for identifying proteins or
for homologous nucleic acids required for cellular proliferatio
isolate candidate molecules for rational drug discovery program
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                                      Ohlsen
Forsyth
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                                      Haselbeck R
Yamamoto R,
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 PHARM INC.
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JB,
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B; ACA44115.
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Trawick
 ELITRA
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 (ELIT-)
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of

475 AA; Sequence

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Gaps
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 Length 475;
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Score 34; DB 6; Le
Pred. No. 4.6e+02;
0; Mismatches 3;
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Similarity 57.1%; 4; Conservative (
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standard; protein; ABU29756; ABU29756 RESULT 10 ABU29756 ID ABU2 

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encoded by Prokaryotic essential gene #15283 Protein

entry)

(first

19-JUN-2003

drug gene; cell proliferation; essential Antisense; prokaryotic

Enterococcus faecium.

WO200277183-A2

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the folly antisense to an isolateu nucleic acid comprising any one of the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid;
(2) a host cell containing the vector; (3) an isolated are:

(1) a vector comprising a promoter operably linked to the nucleic acid;
(2) a host cell containing the vector; (3) an isolated artisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway contained for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotis; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for cellular proliferation to isolate candidate molecules for rational changing accepting or to a for screening homologous nucleic acide required for any discoverty programs, or for screening homologous nucleic acide acide action of an organism. The antisense molecules acide acide action of an organism acts; (11) accepting nucleic acide acide action of an organism acts; (11) accepting acceptin
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Trawick
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                                                                                                     25-OCT-2001;
08-FEB-2002;
06-MAR-2002;
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                                                                                       6-SEP-2001;
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Wall D,
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ADS24700
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promoter functions are recombinant DNA construct comprising a promoter functional in a plant pell, where the promoter is positioned to promoter functional in a plant pell, where the promoter is positioned to converte for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant. DNA construct and a method of producing a craps plant countries and property. The plant is a crop plant comprised property comprises transforming a plant with the having an improved property comprises transforming a plant with the combinant DNA construct and growing the transformed plant where the polymucleotide or polypeptide is useful for improving plants with improved plant properties, e.g. improved cold, heat or drought tolerance.

The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance.

The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance.

The resistance to harbicides, extreme osmotic conditions, pathogens or pests, or or existance to plant disease, better growth rate by modification of carbohydrate, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved plant growth and development under at least one stress providing improved plant growth and development under at least one stress condition, improved plant growth and development of photosynthesis or by production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not format from mean transferment from mean from mean format from mean from the promoted of the growth recombined by the growth recombined by the printed specification of the growth format for the sequence data for this patent did not format from the properties of the properties of the plant growth recombined by the plant growth reco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to provide
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                                                                       property;
osmosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   improved pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoter positioned a polypeptide from its with improved pro
                                                            Recombinant DNA construct; transformed plant; improved plant cold tolerance; heat tolerance; drought tolerance; herbicide; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbinitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from USPTO at segdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 8; L4
Pred. No. 4.6e+02;
; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant DNA construct comprising a profor expression of a polynucleotide encoding a microbial source, useful for producing plants
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ilarity 57.1%;
Conservative
                                     Bacterial polypeptide #13733.
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  entry)
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  (first
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HINKLE
SLATER
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 02-DEC-2004
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Matches 4
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                                                                                                                                                                                                                                      Bacteria
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The present invention relates to novel Streptococcus agalactiae
nucleotide sequences (1; ADV87607-ADV87745) and novel polypeptides of S.
ADV87746-ADV89950). The nucleotide sequences encode polypeptides of S.
cagalactiae involved in the synthesis of amino acids, cell membranes,
intermediate (central) metabolism, energetic metabolism, fatty acid and
phospholipid metabolism, nucleotide metabolism including purines,
pyrimidines and/or nucleosides, regulatory functions, replication,
conditions, sensitivity to medicines and/or analogues, functions related
to transposons, biosynthesis of cofactors, prosthetic groups and
transporters, cell membrane proteins and cellular machinery. (I) are
useful for the detection and/or amplification of nucleic acids.
Charmaceutical composition comprising (I) or (II) are useful for
treatment of a bacterial S. agalactiae infection. Note: WO200292818A2
contains 6617 sequence whereas the present patent only contains 2344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     related
                                                                                                                                                                                                                                                                                                                                                                                                                   nucleotide sequences encoding polypeptides of Streptococcus
iae for the development of vaccines, diagnostic tools, DNA chips
atification of therapeutic targets.
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Poyart C, Trieu CP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 8;
Pred. No. 4.6e+02;
; Mismatches 3
                                                                                                          SEQ
                                                                                                                                   Vaccine; bacterial infection
                                                                                                           Streptococcus agalactiae protein sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; SEQ ID NO 300; 2687pp; French
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                         standard; protein; 475
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57.1%;
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                                                                                 (first entry)
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Couve E,
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(CNRS ) CNRS
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Zouine
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Matches
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RESULT 12
ADV87906
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                                                                                                                                                                                                                    Genomic nucleotide sequences encoding polypeptides of Streptococcus agalactiae for the development of vaccines, diagnostic tools, DNA chipand identification of therapeutic targets.
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Pred. No. 4.6e+02;
          SEQ ID 2497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus agalactiae protein, SEQ ID 300
                            Antibacterial; vaccine; bacterial infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infection
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          Streptococcus agalactiae protein,
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R. Buchrieser
                                                                                                                                                                       Chevalier
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                                                                                                                                                    CENT NAT RECH SCI
                                                                                                     2002WO-IB003059
                                                                                                                         2001FR-00005642
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57.1%;
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                                               Streptococcus agalactiae.
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                                                                                                                                                                                                                                                            SEQ ID NO 2497;
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                                                                                                                                            PASTEUR.
                                                                                                                                                                      Rusniok (
Couve E,
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                                                                 WO200292818-A2
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                                                                                                                                          ) INST
                                                                                                     26-APR-2002;
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                                                                                    21-NOV-2002
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Zouine M,
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Best Local
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The present invention relates to novel Streptococcus agalactiae nucleotide sequences (I; ADV78860-ADV78998 and ADV83341-ADV85476) and novel polypeptides (II; ADV78999-ADV81203 and ADV81205-ADV83340). The nucleotide sequences encode polypeptides of S. agalactiae involved in the synthesis of amino acids, cell membranes, intermediate (central) metabolism, energetic metabolism, fatty acid and phospholipid metabolism, nucleotide metabolism including purines, pyrimidines and/or nucleosides, regulatory functions, replication, transcription, translation, protein transport, adaptation to atypical conditions, sensitivity to medicines and/or analogues, functions related to transposons, biosynthesis of cofactors, prosthetic groups and transporters, cell membrane proteins and cellular machinery. (I) are useful for the detection and/or analogues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cofactors, prosthetic groups and transporters, cell membrane proteins and cellular machinery. (I) are useful for the detection and/or amplification of nucleic acids. Pharmaceutical composition comprising (I) or (II) are useful for treatment of a bacterial S. agalactiae infection. The complete genome of Streptococcus agalactiae is given in ADV81204. Note: The present patent is an equivalent for the basic patent FR2824074Al, which contains only 2344 sequences.
                                                                                                                                                                                                                                                                                                      Genomic nucleotide sequences encoding polypeptides of Streptococcus agalactiae for the development of vaccines, diagnostic tools, DNA chips and identification of therapeutic targets.
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Poyart C, Trieu-Cuot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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98US-0085598P
                                          2002WO-IB003059
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Couve E,
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                                                                                                                                INST
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; SEQ
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                                                                                     26-APR-2001;
                                             26-APR-2002;
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14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US6583275-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUN-2003.
21-NOV-2002
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Zouine M,
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(CNRS )
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us-10-046-922-67

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New isolated nucleic acid derived from Enterococcus faecium encoding
Enterococcus faecium polypeptide useful for detection, prevention and
treatment of a pathological condition resulting from a bacterial
                                                                                       243pp; English
      CORP
      GENOME THERAPEUTICS
                    Bush D;
                                                                                       1; SEQ ID NO 6868;
                                 WPI; 2003-799836/75
N-PSDB; ADC93587.
                    Doucette-Stamm LA,
                                                                                          Example
       (GENO-)
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The invention relates to an isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide having Enterococcus faecium encoding an Enterococcus faecium polypeptide having cone of 10 fully defined sequences given in the (or comprising 40 sequential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid The nucleic acids are chosen from 3654 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids is useful for diagnosing pathological conditions infection, bacteraemia, endocarditis, wounds and abdominal-pelvic infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans derived peptides or antisense polypeptides. Pharmaceutical compositions and vaccines containing the nucleic acid are useful for preventing or treating Enterococcus faecium infections. The present sequence represents cone if the disclosed E. faecium proteins.

Sequence 478 AA;

0 Length 478; Indels Score 34; DB 7; Le Pred. No. 4.7e+02; 0; Mismatches 3; Similarity 57.1%; 4; Conservative Query Match Best Local Best Loc Matches

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104 98 GYWLSAW 2006, 08:54:55 2, completed: May : time Search Job tim

qq

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version 5.1.7 - 2006 Biocceleration Ltd
GenCore (c) 1993
             Copyright
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using sw model protein search, OM protein 08:47:12 2, 2006, May Run on:

; Search time 12.6977 Seconds
 (without alignments)
53.043 Million cell updates/sec

US-10-046-922-67 35 1 GYWXXXW 7 Title: Perfect

score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table

96216763 residues 283416 segs, Searched: of hits satisfying chosen parameters: Total number

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

•• Database

IR\_80:\* pir1:\* pir2:\* pir3:\* чሪ w 4

printed, Ø pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being piand is derived by analysis of the total score distribution. score gand is

#### SUMMARIES

Description	ypothetical pr	ypothetical prot	othetical prot	ransporter	ble amino ac	ine/ornithi	ine/ornithin	ne/ornitin	ine/ornitine	avy chain pr	acylglycerol	hetical pro	peptide ABC	hetical prot	ble transpor	ble ABC tran	hetical prot	ole carbohyd	othetical prot	ble dipeptid	thetical prot	othetical pro	A protein [imp	pothetical prot	etical prot	ltidrug res	sis protein S -	oothetical prot	cal pro
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218 2518 2611 2611 2711 282 344 448 516 519	631
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Η.
	32
К В В В В В В В В В В В В В В В В В В В	45

# ALIGNMENTS

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hypothetical protein 72B - rice mitochondrion
hypothetical protein 72B - rice mitochondrion
C; Species: mitochondrion Oryza sativa (rice)
C; Species: mitochondrion Oryza sativa (rice)
C; Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C; Accession: T03190
R; Itadani, H: Wakasugi, T:; Sugita, M.; Sugiura, M.; Nakazono, M.; Hirai, A.
R; Italeani, H: Wakasugi, T:; Sugita, M.; Sugiura, M.; Nakazono, M.; Hirai, A.
Plant Cell Physiol. 35, 1239-1244, 1994
A; Title: Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA: the existe
A; Reference number: Z14841; MUD:95211382; PMID:7545979
A; Reference roundry; translated from GB/EMBL/DDBJ
A; Access: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-72 <ITA>
A; Stacusion: T03190
A; Stacusion: UNIPROT:Q35302; UNIPARC:UPI00009746F; EMBL:D32052; NID:9769704; F
A; Experimental source: cultivar Nipponbare
C; Genetics:
A; Genome: mitochondrion
C; Keywords: mitochondrion
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0; Mismatches
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4; Conservative
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Matches 4
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RESULT S12193

hypothetical protein 4 - Thiobacillus ferrooxidans plasmid pTF1
C;Species: Thiobacillus ferrooxidans
C;Species: Thiobacillus ferrooxidans
C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004
C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004
C;Accession: S12193
R;Drolet, M.; Zanga, P.; Lau, P.C.K.
Mol. Microbiol. 4, 1381-1391, 1990
A;Title: The mobilization and origin of transfer regions of a Thiobacillus ferrons. S12193
A;Reference number: S12188; MUID: 91125140; PMID: 2280689
A;Accession: S12193
A;Accession: S12193
A;Ctatus: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <DRO>
A;Cross-references: UNIPROT: P20088; UNIPARC: UPI000013B9EC; EMBL: X52699; NID: 9486
C;Genetics:
A;Genome: plasmid pTF1

ferrooxidan

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EMBL:X52699; NID:948158; ô Gaps ö Length 108 2; Score 34; DB Pred. No. 21; 0; Mismatches 97.1%; illarity 57.1%; Conservative Query Match Best Local Similarity

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                                                    (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arginine/ornithine antiporter [imported] - Lactobacillus sakei
C;Species: Lactobacillus sakei
C;Species: Lactobacillus sakei
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-Oct-2004
C;Accession: T46745
R;Zuniga, M.; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; Perez-Mirtie: Structural and functional analysis of the gene cluster encoding the en;
A;Title: Structural and functional analysis of the gene cluster encoding the en;
A;Reference number: Z23141; MUID:98361904; PMID:9696763
A;Recession: T46745
A;Recession: T46745
A;Residues: 1-475 <ZUN>
A;Molecule type: DNA
A;Residues: 1-475 <ZUN>
A;Residues: 1-475 <ZUN>
A;Gene: arcD
C;Genetics:
A;Gene: arcD
C;Function: necessary for arginine transport; involved in ornithine-arginine
A;Pathway: arginine catabolism
C;Superfamily: ecotropic retrovirus receptor protein
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                                                                                                         #text_change 05-Oct-2004
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                                                    Pseudomonas aeruginosa
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                                                                                                                                                                                                                           .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PAO1,
A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Accession: E83497
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-472 <STO>
A; Experimental source: strain PAO1
C; Genetics:
A; Gene: PA1194
C; Superfamily: ecotropic retrovirus receptor protein
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                                  probable amino acid permease PAl194 [imported] - Ps C; Species: Pseudomonas aeruginosa C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 C; Accession: E83497 R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, adman, S.; Yuan, Y.; Brody, L.L.; Coulter S.N. Fr
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79;
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Lory, S.; Olson, M.V.
.ure 406, 959-964, 2000
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C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
C;Accession: D70048
R;Kunst, F: Ogasawara, N: Moszer, I: Albertini, A.M.; Alloni, G: Azevedo, V: Berter
C; Bron, S: Brouillet, S: Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Enrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, X.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Hibert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogivara, A.; Oudega, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Yamanoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A;Authors: Yoshikawa, H.F.; Zumstein, A;Authors: Yoshikawa, H.F.; Zumstein, A;Authors: Yoshikawa, H.F.; Zumstein, A;Authors: Yoshikawa, H.F.; Zumstein, A;Authors: Voshikawa, H.F.; Zumstein, A;Authors: Voshikawa, H.F.; Zumstein, A;Authors: Voshikawa, H.F.; Zumstein, Bacillus subtilis.
A;Reference number: A69580; MUD:98044033; PMID:9384377
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                                                                                                                                                            hypothetical protein SCJ9A.03c - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-C; Accession: T37139

R; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M submitted to the EMBL Data Library, August 1999

A; Reference number: Z21622

A; Reference number: Z21622

A; Reference number: Z21622

A; Residues: preliminary; translated from GB/EMBL/DDBJ

A; Residues: 1-345 < HAR>
A; Residues: 1-345 < HAR>
A; Residues: 1-345 < HAR>
A; Cross-references: UNIPROT: Q9S1R7; UNIPARC: UPI0000DB3A4; EMBL: AL10997

A; Experimental source: strain A3(2)
C; Genetics:
A; Gene: SCOEDB: SCJ9A.03c
C; Superfamily: Streptomyces coelicolor hypothetical protein SCJ9A.03c
                                                                                                                                                                                                                                                                                      B.G.; Rajandream,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30
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C; Genetics: A; Gene: yvsH
C; Superfamily: ecotropic retrovirus receptor protein
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Pred. No. 59;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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|-|| |
89 GYWRSSW 95
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Best Local Similarity
Matches 4; Conser
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PID:912725079;

GB: AE005176;

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C;Species: Wycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S73905
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoni A;Reference number: S73327; MUID:97105885; PMID:8948633
A;Residues: 1-227 <HIM>A;Residues: 1-227 <HIM>A;R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 1
C; Accession: C34903
R; Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A; Title: Active site structure and antigen binding properties of A; Title: Active site structure and antigen binding properties of A; Reference number: A34903; MUID:90094387; PMID:2104617
A; Reference number: A34903; MUID:90094387; PMID:2104617
A; Reference number: A34903; MUID:90094387; PMID:2104617
A; Residues: 1-142 < BED>
A; Cross-references: UNIPARC:UPI0000176C0F
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-119/Domain: immunoglobulin homology < IMM>
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873905
CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase
N;Alternate names: hypothetical protein A65_orf227
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                 UNIPARC: UPI00000C6B95;
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Pred. No. 39;
0; Mismatches
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ed. No. 82;
Mismatches
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Pred. No.
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                   source: strain IL1403
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ilarity 57.1%;
Conservative
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illarity 57.1%;
Conservative
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                          ferences:
A;Residues: 1-49
A;Cross-referenc
A;Experimental 8
C;Genetics:
A;Gene: arcD2
C;Superfamily: 6
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Best Local S
Matches 4
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Best Local S
Matches 4
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                                                       .NID:9151030;
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P.; Hickey,
A.; Larbig,
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  A; Molecule type: DNA
A; Residues: 1-482 <LUE>
A; Cross-references: UNIPROT:P18275; UNIPARC:UPI0000618AA; GB:M33223; NID:g15
A; Cross-references: UNIPROT:P18275; UNIPARC:UPI0000618AA; GB:M33223; NID:g15
A; Experimental source: strain PAO1
A; Note: the gene encoding this protein is located upstream of the arcABC gene R; Stover, C. K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hicke adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbi, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportun A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Reference number: A82959
A; Status: preliminary
A; Molecule type: DNA
A; Status: preliminary
A; Molecule type: DNA
A; Status: L482 <STO>
A; Experimental source: strain PAO1
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: ecotropic retrovirus receptor protein
C; Keywords: transmembrane protein
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A; Title: The complete genome sequence of the lactic acid bacterium Lacto A; Reference number: A86625; MUID:21235186; PMID:11337471

A; Recession: C86879

A; Residues: L-490 <STO>
A; Residues: 1-490 <STO>
A; Residues: 1-490 <STO>
A; Experimental source: strain IL1403
C; Genetics:
A; Experimental source: strain IL1403
C; Genetics:
A; Genetics:
A; Coss-references: arcbl
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Pred. No. 81;
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Pred. No. 8
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ilarity 57.1%;
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A;Status: preliminary
A;Molecule type: DNA
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oligopeptide ABC transporter, permease protein - Thermotoga maritima (strai)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: G72215
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Ri
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A; Title: Evidence for lateral gene transfer between Archaea and Bacte A; Reference number: A72200; MUID:99287316; PMID:10360571
A; Accession: G72215
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-289 <ARN>
A; Residues: 1-289 <ARN>
A; Cross-references: UNIPROT:Q9X270; UNIPARC:UPI00000D385E; GB:AE00187; C; Genetics:
A; Experimental source: strain MSB8
C; Genetics:
A; Gene: TM1748
C; Superfamily: oligopeptide permease protein oppB
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hypothetical protein all1931 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Nostoc sp. strain PCC 7120
A;Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AE2047
C;Accession: AE2047
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch.
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda,
Na, Sille: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ar.
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Status: preliminary
A;Molecule type: DNA
A;Status: preliminary
A;Cessereferences: UNIPROT:QSYVP3; UNIPARC:UPI00000CE269; GB:BA000019; PIDN:BAB73630.1
A;Experimental source: strain PCC 7120
C;Genetics:
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Search completed: May 2, 2006, 08:56:19 Job time : 12.6977 secs

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Biocceleration Ltd
GenCore version (c) 1993 - 2006
              Copyright
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using sw model protein search, OM protein

08:38:27 2006, 7 May Run on:

; Search time 79.2791 Seconds
 (without alignments)
 62.295 Million cell updates/sec

US-10-046-922-67 35 Perfect score: Title

~ 1 GYWXXXW Sequence:

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705528306 residues 2166443 seqs, Searched:

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UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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# ALIGNMENTS

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NUCLEOTIDE SEQUENCE.
MEDLINE=95211382; PubMed=7545979;
Itadani H., Wakasugi T., Sugita M., Sugiura M., Nakazono M., Hirai A.;
"Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA:
the existence of many sequences that correspond to parts of
mitochondrial genes in intergenic regions.";
Plant Cell Physiol. 35:1239-1244(1994).
EMBL; D32052; BAA06811.1; -; Genomic_DNA.
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                                                                                            Oryza gativa (japonica cultivar-group).
Mitochondrion.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta.
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
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MEDLINE=95308541; PubMed=7788722; DOI=10.1007/BF00313433;
Nakazono M., Itadani H., Wakasugi T., Tsutsumi N., Sugiur
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Baev A.A., Dzhumagaliev E.B.,
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                                                                                                                                                                                         [us
                                                                                                                                           NUCLEOTIDE SEQUENCE [GENOMIC DNA].

STRAIN=ATCC 33020;

MEDLINE=91125140; PubMed=2280689;

Drolet M., Zanga P., Lau P.C.K.;

"The mobilization and origin of transfer regions of a Thiobacilly ferrooxidans plasmid: relatedness to plasmids RSF1010 and pSC101 for Microbiol. 4:1381-1391(1990).
                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillal
Acidithiobacillaceae; Acidithiobacillus.
NCBI_TaxID=920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MED4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
MEDLINE=22825698; PubMed=12917642; DOI=10:1038/nature01947;
Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P., Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R., Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A., Webb E.A., Zinser E.R., Chisholm S.W.; "Genome divergence in two Prochlorococcus ecotypes reflects oceaniche differentiation.";
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                                                                                                                                                                                                                                  ss-Prot entry is copyright. It is produced through a the Swiss Institute of Bioinformatics and the EMBI pean Bioinformatics Institute. There are no restricting as its content is in no way modified and this standard
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                                                                                                                                                                                                                                                                                                                                                          Length 108
                                                                                                                                                                                                                                                                                                                                                                               Indels
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Possible Adenoviral fiber protein (Repeat/shaf).
OrderedLocusNames=PMM1067;
                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 1; Lo
Pred. No. 1.8e+02;
0; Mismatches 3;
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          or-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Hypothetical 12.3 kDa protein in mobL 3'region
Thiobacillus ferrooxidans.
Plasmid pTF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 AA
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                                                                                                                                                                                                                                                                                                  CAA36930.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                 EMBL, X52699, CAA36930.1; -; Ge
PIR, S12193; S12193.
Hypothetical protein; Plasmid.
SEQUENCE 108 AA; 12335 MW;
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EMBL; BX572092;. CAE19526.1;
Complete proteome.
SEQUENCE 130 AA; 14024 MV
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4; Conservative
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larity 57.1%;
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395_PROMP
Q7U395_PROMP_PRELIMINARY;
Q7U395;
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in perinatal human immunodeficiency virus (HIV) type 1 transmission:
the ariel project for the prevention of transmission of HIV from
                                                                                                                                                           Orthoretrovirinae;
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MEDLINE=99214336; PubMed=10196293;
Wilson C.C., Brown R.C., Korber B.T., Wilkes B.M., Ruh
Sakamoto D., Kunstman K., Luzuriaga K., Hanson I.C., W
Wiznia A., Clapp S., Ammann A.J., Koup R.A., Wolinsky
Walker B.D.;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update) .
01-JUN-2003 (TrEMBLrel. 24, Last annotation update) .
Arginine/ornithine antiporter homolog ArcD (Fragment) .
Name=arcD; .
Lactococcus lactis (subsp. cremoris) (Streptococcus c
                                                           Last sequence update)
Last annotation update)
                                                                                                                                                           Retroviridae;
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3.7e+02;
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Pred. No.
                                                                                                                                      Human immunodeficiency virus 1.
Viruses; Retro-transcribing viruses;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
                                       Created)
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PRT;
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27062 MW;
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J. Virol. 73:3975-3985(1999).
EMBL; AF121641; AAD29013.1; -;
HSSP; P03366; 1HRH.
SMR; Q9WGW9; 1-236.
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iilarity 57.1%;
Conservative (
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032816;
 9HIV1 PRELIMINARY;
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(TrEMBLrel. )
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15514110; DOI=10.1093/nar/gkh910;
., Vallenet D., Fonknechten N., Kreimeyer A., Oztas S.,
L., Cruveiller S., Robert C., Duprat S., Wincker P.,
L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;
features revealed by the genome sequence of Acinetobacter sp
versatile and naturally transformation competent bacterium."
Acids Res. 32:5766-5779(2004).
R543861; CAG70223.1; -; Genomic_DNA.
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STRAIN=A3(2) / M145;
STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
MEDLINE=21996410; PubMed=120.1038/417141a;
MEDLINE=21996410; PubMed=120.1038/417141a;
Medline A., Kieser H., Hobele A., Moodward J.R., Barrell B.G., Parkhill
                                                                                                    Acinetobacter sp. (strain ADP1).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales
Moraxellaceae; Acinetobacter.
NCBI_TaxID=62977;
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09S1R7.
Cystrco
09S1R7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein SC00224.
OrderedLocusNames=SC00224; ORFNames=SCJ9A.03c;
Streptomyces coelicolor.
Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                            update)
acid transporter
                                                                                                                                                                                                                                                                                                                                                                                      activity; IEA
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23643009936285B8 CRC64
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(TrEMBLrel. 27, Last sequence update)
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Pred. No. 5e+02;
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GO; GO:0008508; F:bile acid:sodium symporter
GO; GO:0006814; P:sodium ion transport; IEA.
InterPro; IPR002657; BilAc/Na_symport.
Pfam; PF01758; SBF; 1.
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NCBI_TaxID=1902;
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                                                             Putative transporter; putative
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Warren T.,
Hopwood D.A.;
"Complete genome seq.
coelicolor A3(2).";
Nature 417:141-147(2002).

EMBL; AL939104; CAB53264.1;
PIR; T37139; T37139.
Tlete proteome; Hypothetic
a45 AA; 36929 MW
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ilarity 57.1%;
Conservative
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OrderedLocusNames=ACIAD3583
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Barbe V., Vallenet
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             05-JUL-2004
05-JUL-2004
05-JUL-2004
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                                                                                                                                                                                                     NUCLEOTIDE
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Complete
SEQUENCE
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     occus
                                                                STRAIN=MG1363;

MEDLINE=97369814; PubMed=9226255;

MEDLINE=97369814; PubMed=9226255;

Duwat P., Cochu A., Ehrlich S.D., Gruss A.;

Characterization of Lactococcus lactis UV-sensitive mutants obta is acteriol. 179:4473-4479(1997).

By ISSI transposition.";

J. Bacteriol. 179:4473-4479(1997).

R AC45504.1; -; Genomic_DNA.

R GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005279; F:amino acid-polyamine transporter activity; IEP.

R GO; GO:0006865; P:amino acid-polyamine transporter activity; IEP.

R GO; GO:0006865; P:amino acid transport; IEA.

InterPro; IPR002293; AA/rel_permeasel.
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STRAIN=HTE831 / DSM 14371 / JCM 11309;
MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from Ridge and its unexpected adaptive capabilities to extreme environments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 294;
                                                                                                                                                                                                                                                                                                                                              253;
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Nucleic Acids Res. 30:3927-3935(2002).

EMBL; BA000028; BAC12390.1; -; Genomic_DNA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:00042626; F:ATP binding; IEA.

GO; GO:0006810; P:transport; IEA.

InterPro; IPR001626; ABC_3.

InterPro; IPR001626; ABC_3.

Complete proteome; Transmembrane; Transport.

SEQUENCE 294 AA; 31323 MW; F75E50F22EA4071A CRC64;
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     Streptococcaceae;
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ed. No. 3.9e+02;
Mismatches 3
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Pred. No. 4.5e+02;
Mismatches
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OrderedLocusNames=OB0434;
Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae;
NCBI_TaxID=182710;
                                                                                                                                                                                                                                                                                                                                             Score 34;
Pred. No. 3
Bacteria; Firmicutes; Lactobacillales;
NCBI_TaxID=1359;
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Best Local Similarity 57.1%,
Matches 4; Conservative
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QBET30;
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
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der H., Collins M., Howarth S., (., O'Neil S.,

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STRAIN=ATCC 23344;

Rubmed=15377793; DOI=10.1073/pnas.0403306101;

Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,

Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,

A Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.

A Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,

Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,

A Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.

R Zafar N., Zhou L., Fraser C.M.;

"Structural flexibility in the Burkholderia mallei genome.";

Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).

R TIGR; BMAA1038;

TIGR; BMAA1038;
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
NCBI_TaxID=13373;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
NCBI_TaxID=1360;
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0005279; F:amino acid-polyamine transporter
GO; GO:0006865; P:amino acid transport; IEA.
GO; GO:0006810; P:transport; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR002293; AA/rel_permeasel.
InterPro; IPR004841; Permease_region.
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Chou L., Weimer B., Xie Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ
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Q62C74 BURMA PRELIMINARY;
Q62C74;
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
Amino acid permease.
OrderedLocusNames=BMAA1038;
Similarity 57.1%; 4; Conservative
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Chou L.-S., Weimer B., Xie Y.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ da
EMBL; AF282249; AAF86987.1; -; Genomic DNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005279; F:amino acid-polyamine transport
GO; GO:0006865; P:amino acid transport; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR002293; AA/rel_permeasel.
InterPro; IPR004841; Permease_region.
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STRAIN=ATCC 23279;

MEDLINE=22519090; PubMed=12631210;

DOI=10.1046/j.1365-2672.2003.01907.x;

Divol B., Tonon T., Morichon S., Gindreau E., "Molecular characterization of Oenococcus oen involved in arginine transport.";

J. Appl. Microbiol. 94:738-746(2003).

REMBL; AF541253; AAO83382.1; -; Genomic_DNA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0006865; P:amino acid transport; IEA.

GO; GO:0006810; P:transport; IEA.

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utes; Lactobacillales;
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Name=arcD2;
Oenococcus oeni (Leuconostoc Oenor)
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Q84DL5;
01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
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PubMed=15155910; DOI=10.1073/pnas.0402414101;
PubMed=15155910; DOI=10.1073/pnas.0402414101;
Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
A marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
A maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
A Rilstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
A Rilstone J., Fraser C.M.;
Popovic T., Fraser C.M.;
A "Identification of anthrax toxin genes in a Bacillus cereus associ
with an illness resembling inhalation anthrax.";
Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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STRAIN=Sterne;

Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C.,

Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Ok

Richardson P., Rubin E., Tice H.;

Richardson P., Rubin E., Tice H.;

"Complete genome sequence of Bacillus anthracis Sterne.";

"Complete genome sequence of Bacillus anthracis Sterne.";

Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; AE017225; AAT52924.1; -; Genomic DNA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0006865; P:amino acid-polyamine transporter activity.

GO; GO:0006810; P:transport; IEA.

GO; GO:0006810; P:transport; IEA.

InterPro; IPR002293; AA/rel_permeasel.

InterPro; IPR004841; Permease region.
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                                                       Bacillus anthracis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
Bacillus cereus group.
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EMBL; AAEK01000024; EAL13575.1; -; Genomic_DNA.
SEQUENCE 465 AA; 50180 MW; F2A1540B055C90B9 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Arginine/ornithine antiporter.
Name=arcD; ORFNames=BCE_G9241_0606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            core 34; DB 2; Le
red. No. 6.8e+02;
Mismatches 3;
     update)
                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 2; ]
Pred. No. 6.8e+02; ]; Mismatches 3
                                                                                                                         NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            465 AA
  05-JUL-2004 (TrEMBLrel. 27, Last sequence up 05-JUL-2004 (TrEMBLrel. 27, Last annotation Amino acid permease family protein. OrderedLocusNames=BAS0596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
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nembrane; Transport.
ICE 465 AA; 50192 MW;
                                                                                                                                                                                                                                                                                                                                                                                       97.1%;
ilarity 57.1%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q4mns6_BACCE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus cereus G9241.
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Bacillus cereus group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lus cereus group
TaxID=269801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYWAANW 102
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Matches 4; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GYWXXXW
                                                                                                NCBI_TaxID=1392;
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13-SEP-2005
13-SEP-2005
13-SEP-2005
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Best Local S
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BACCE
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Q4MN56
ID Q4
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Gaps
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                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.

NUCLEOTIDE SEQUENCE.

MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;

Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,

Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus
Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,

Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,

Overbeek R., Kyrpides N.C.,

"Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthracis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activity; IEA
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as S.
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                                                                                                                                                                                                              (strain ATCC 14579 / DSM 31).
utes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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C:membrane; IEA.
F:amino acid-polyamine transporter
P:amino acid transport; IEA.
                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transporter
IEA.
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Brettin T.S., Bruce D., Challacombe J.F., Gilna Hitchcock P., Jackson P., Keim P., Longmire J., Richardson P., Rubin E., Tice H.; "Complete genome sequence of Bacillus cereus ZK Submitted (JUL-2004) to the EMBL/GenBank/DDBJ de EMBL; CP000001; AAU19700.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 2; Pred. No. 6.8e+02; 0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9750B5D1019142F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=arcD;
Bacillus cereus (strain ZK).
Bacteria; Firmicutes; Bacillales; Bacillus cereus group.
NCBL TaxID=288681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  $
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 465
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GO; GO: 0005279; F: amino acid-polyamine t
GO; GO: 0006865; P: amino acid transport;
GO; GO: 0006810; P: transport; IEA.
InterPro; IPR002293; AA/rel_permeasel.
InterPro; IPR004841; Permease_region.
Pfam; PF00324; AA_permease; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50040 MW;
                                                           (TrEMBLrel. 24, C
(TrEMBLrel. 24, I
(TrEMBLrel. 26, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 423:87-91(2003).
EMBL; AE017000; AAP07646.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QE3G16_BACCZ PRELIMINARY;
Q63G16;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Bacteria; Firmicutes;
Bacillus cereus group.
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4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ~
                                                                                                                                                                                                                                                                                                        NCBI_TaxID=226900;
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GO: 0016020;
GO: 0005279;
GO: 0006865;
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Gaps

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Indels

0;

GYWXXXW

Matches

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DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR002293; AA/rel_permeasel.

DR InterPro; IPR004841; Permease_region.

DR Pfam; PF00324; AA_permease; 1.

KW Complete proteome; Transmembrane; Transport.

SQ SEQUENCE 465 AA; 50178 MW; 55D7083AAE7B3958 CRC64;
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		Gaps
		0;
ength 465;		Indels
H	2;	'n,
	6.8e+02;	Mismatches
34;	No.	smat
Score 34;	red.	M.
S	<u>α</u>	ó
97.18	57.1%;	ative
	ilarity	Conservative
c.	Simila	4.
· Query Match	Best Local	Matches

Search completed: May 2, 2006, 08:46:46 Job time : 79.2791 secs

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5.1.7
Biocceleration Ltd
 version - 2006
 GenCore (c) 1993
          Copyright
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using sw model protein search, OM protein

•• 08:55:22 2006, 7 May Run on:

Search time 19.8605 Seconds (without alignments) 29.140 Million cell updates/sec

US-10-046-922-67

7 1 GYWXXXW score: Title: Perfect so Sequence: BLOSUM62 Gapop 10.0 , table: Scoring

0.5 Gapext 572060 hits satisfying chosen parameters: of Total number

residues

segs, 82675679

572060

Séarched

2000000000 length: length: seq sed Minimum DB Maximum DB

Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

s a orinted, Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pand is derived by analysis of the total score distribution.

### SUMMARIES

		•			. Control of the cont		
Result No.	Score	.Ouery Match	Length	DB	ID	cript	
-	4.5	97.1	1 [	2 !	-107-532A-686	equence 6868,	
, 0	) K	97.1	· Ø	2	-09-252-991A-2332	equence 23328,	
1 m	) W	97.1	865	~	8-09-252-99	equence	
) 4	, W	94.3	4	7	-252-991A-1869	e 18697,	
· LO	. E	94.3	49	7	-09-792-616-	equence 9, App	
Φ.	33	₹*	0	~	-09-792-616-	equence 3, App	
7	9 69	-	50	7	-09-647-1	ence 8, App	
<b>c</b> c	32	н	æ	7	-902-540-1	equence 12675,	
9	32	-	~	7	-09-543-681A-762	equence 7620,	
10	32	_	ហ	7	-502-653-	equence 10, Ap	
1	32	91.4	φ	7	-009-610-906-1	equence 12, Ap	
175	35	-	_	7	-09-248-796	equence 15791,	
13	32	Н	~	~	-145-828A-1	equence 11, Ap	
14	32	91.4	~	7	-09-903-45	equence 18, Ap	
15	32	$\boldsymbol{\vdash}$	7	~	-09-624-670-1	equence 17, Ap	-
16	32	$\boldsymbol{H}$	ന	~	-252-99	equence 26841,	
17	32	_	9	Н	-08-415-7	equence 6, Apr	
18	. 32	_	9	~	-248-796	equence 15188,	
19	32	91.4	492	7	-09-107-532A-	equence 6945,	
20	32	$\leftarrow$	0	7	-09-252-991A-212	equence 21214,	
21	31	œ	œ	7	-808-807-12	equence 12, Ap	
22	31	B	4	~	-09-252-991A-	equence 32031,	
23	30	S	11	7	-069-827A-8	equence 87, Ap	
24	30	S	16	C¥	9-620-091-81	equence 81, Ap	
25	30	ß	_	7	-09-198-452A-	equence 479, F	
26	30	85.7	519	~	-09-438-185A-454	ence 454, F	
27	30	S	S	7	US-09-252-991A-18441	equence 18441,	
		•					

; LOCATION: (B) LOCATION 1...478 ; SEQUENCE DESCRIPTION: SEQ ID NO: 6868 US-09-107-532A-6868

Enterococcus faecium

equence 9656, A	Sequence 1516, Ap	equence 60715,	equence 1191, A	Sequence 1191, Ap	equence 1191, A	equence 1191, A	equence 1191, A	equence 1191, A	equence 7633, A	equence 7239, A	equence 19685,	equence 22994,	equence 5312, A	equence 8752	equence 45223,	9		
	5	-09-270-767-60	-09-082-279B-11	-09-315-304B-11	US-09-834-784-1191	US-09-515-965A-1191	US-09-350-641C-1191	US-09-350-841A-1191		-09-621-976-723	-09-252-9	-09-252-991A-229	US-09-543-681A-5312	-09-489-039A-875	-09-270-767-4522	US-09-712-363-168	US-10-272-490-62	
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28	600	. C		32	1 E	3.6	32.	36	37	3.8	6 E	0 4	41	. 42	, 4 1 K	4 4	45	

## ALIGNMENTS

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and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                              THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 30-Jun-1998
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTC-012
                                                                             APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                    ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
            Sequence 6868, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: (781)893-5007
(781)893-8277
) ID NO: 6868:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                        STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME TH
STREET: 100 Beaver S
CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: YES
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                                                                                                                                          SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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-09-107-532A-6868
                                                                                                                                            OF
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Sequence 18697, Application US/09252991A
Sequence 18697, Application US/09252991A
Sequence 18697, Application US/09252991A
Sequence 18697, Application US/09252991A
Better No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18697
LENGTH: 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nutations in a gene encoding an ABC
Pseudoxanthoma Elasticum
                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 2; 1
Pred. No. 3.1e+02;
); Mismatches 3;
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Pred. No. 7.5e+02;
); Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/09792616;
Patent No. 6780587;
GENERAL INFORMATION:
APPLICANT: PXE International, Inc.
APPLICANT: University of Hawaii
TITLE OF INVENTION: Mutations in a gene encoding;
TITLE OF INVENTION: Pseudoxanthoma Elasticum;
FILE REFERENCE: PXE-001
CURRENT APPLICATION NUMBER: US/09/792,616
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: PXE International, Inc.
APPLICANT: University of Hawaii
TITLE OF INVENTION: Mutations in a gene encorrith of Invention: Pseudoxanthoma Elasticurine Reference: PXE-001
CURRENT APPLICATION NUMBER: US/09/792,616
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
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Sequence 3, Application US/09792616
Patent No. 6780587
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                 94.3%;
larity 57.1%;
Conservative
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Similarity 57.1%;
4; Conservative
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CRGANISM: Mus musculus
US-09-792-616-9
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LENGTH: 1498
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US-09-792-616-9
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TYPE: PF
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US-09-792
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US-09-252-991A-19339
i Sequence 19339, Application US/09252991A
patent No. 6551795
i GENERAL INFORMATION:
i APPLICANT: Marc J. Rubenfield et al.
i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TY TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
i FILE REFERENCE: 107196.136
i CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
i PRIOR PILING DATE: 1998-02-18
i PRIOR PILING DATE: 1998-02-18
i PRIOR FILING DATE: 1998-07-27
i NUMBER OF SEQ ID NOS: 33142
i LENGTH: 865
i LENGTH: 865
                                                                                                                                                                    RESULT 2
US-09-252-991A-23328
; Sequence 23328, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: ABOUGHER: US/09/252,991A
; TITLE OF INVENTION: ABOUGHER: US/09/252,991A
; CURRENT APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23328
; LEGGTH: 499
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 Score 34; DB 2; Ler
Pred. No. 1.9e+02;
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Pred. No. 3.1e+02;
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Pred. No.
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Query Match
Best Local Similarity
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Best Local Similarity
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Query Match
Best Local Similarity
US-09-902-540-12675
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US-09-502-653-10
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SENGTH: 252
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US-09-902-540-12675
; Sequence 12675, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses The FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 12675
; LENGTH: 88
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                                                                                                                                                                                                                                                                                               APPLICANT: Kruh, Gal,
APPLICANT: Lee, Kun
APPLICANT: Lee, Kun
APPLICANT: Belinsky, Martin G.
APPLICANT: Bain, Lisa J.
TITLE OF INVENTION: MRP-Related ABC Transporter Enc
TITLE OF INVENTION: Nucleic Acids and Methods of I
FILE REFERENCE: FCCC 98-02
CURRENT APPLICATION NUMBER: US/09/647,140B
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/079,759
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 33
COFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 7
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GENERAL INFORMATION:
APPLICANT: Fox Chase Cancer Center APPLICANT: Kruh, Gary D.
APPLICANT: Lee, Kun
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nilarity 57.1%;
Conservative (
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illarity 57.1%;
Conservative
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                                                   Homo sapiens
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        SEQ ID NO 3
LENGTH: 1503
TYPE: PRT
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US-09-543-681A-7620

Sequence 7620, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09
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Length 88;
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No. 2.3e+02;
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  DB
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APPLICANT: Schlein, Martin
APPLICANT: Schlein, Martin
APPLICANT: Bech, Lisbeth
APPLICANT: Stergaard, Peter Rahbek
APPLICANT: Stergaard, Peter Rahbek
APPLICANT: Sj holm, Carsten
TITLE OF INVENTION: NOVEL GALACTANASES
FILE REFERENCE: 5481.200-US
CURRENT APPLICATION NUMBER: US/09/502,653
CURRENT FILING DATE: 2000-02-11
EARLIER APPLICATION NUMBER: PA 1999 00799
EARLIER FILING DATE: 1999-02-11
EARLIER APPLICATION NUMBER: 60/125,885
EARLIER FILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 52
               94;
                                 Mismatches
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Pred. No.
 Score 32;
Pred. No.
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APPLICANT: Bj rnvad, Mads Eskelned; APPLICANT: Clauser
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Clausen, Ib Groth
Schlein, Martin
Bech, Lisbeth
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ilarity 57.1%;
Conservative
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SEQ ID NO 7620
LENGTH: 177
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  91.4%;
57.1%;
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US-09-543-681A-7620
                   Similarity 57.7
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US-09-502-653-10
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Pred. No. 2.5e+02;
; Mismatches 3;
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; Patent No. 6677145
; GENERAL INFORMATION:
    APPLICANT: Abbott Laboratories
    APPLICANT: Mukerji, Pradip
    APPLICANT: Leonard, Amanda Eun-Yeong
    APPLICANT: Leonard, Amanda Eun-Yeong
    APPLICANT: Huang, Yung-Sheng
    APPLICANT: Pereira, Suzette L.
    TITLE OF INVENTION: ELONGASE GENES AND USES TH:
    FILE REFERENCE: 6407.US.P3
    CURRENT APPLICATION NUMBER: US 09/624,670
    PRIOR APPLICATION NUMBER: US 09/379,095
    PRIOR FILING DATE: 2000-07-24
    PRIOR FILING DATE: 1999-08-23
    PRIOR FILING DATE: 1999-08-23
    PRIOR APPLICATION NUMBER: US 09/145,828
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                                                                                                                                               APPLICANT: Parker-Barnes, Jennifer M.
TITLE OF INVENTION: THE ELONGASE GENE AND
FILE REFERENCE: 6407.US.01
CURRENT APPLICATION NUMBER: US/09/145,828A
CURRENT FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS.
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Pred. No.
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NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version
                           Application US/09145828A 03349
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US-09-624-670-17
; Sequence 17, Application US/09624670
                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Caenorhabditis elegans
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                                                                           Abbott Laboratories
Mukerji, Pradip
Leonard, Amanda E.
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FastSEQ for Windows
                                                                                                                         Huang, Yung-Sheng
Thurmond, Jennifer
Kirchner, Stephen
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                                                                                         APPLICANT: Mukerji,
APPLICANT: Leonard,
APPLICANT: Huang, Yu
APPLICANT: Thurmond,
APPLICANT: Kirchner,
APPLICANT: Parker-Bartille OF INVENTION:
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Best Local Similarity
Matches 4; Conser
                                               Patent No. 6403349
GENERAL INFORMATION:
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RESULT 13
US-09-145-828A-11
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SEQ ID NO 11
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TH: 278
                               Sequence 11,
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US-09-248-796A-15791
US-09-248-796A-15791

; Sequence 15791, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND.AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
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Pred. No. 2.4e+02
  Mismatches
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                                                                                                                                                                                                         APPLICANT: Volkmuth, Wayne
APPLICANT: Klinger, Tod M.
TITLE OF INVENTION: AQUAPORIN-8 VARIANT
FILE REFERENCE: PC-0012 CIP
CURRENT APPLICATION NUMBER: US/09/610,906
CURRENT FILING DATE: 2000-07-06
PRIOR APPLICATION NUMBER: 09/226,994
PRIOR FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 12
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PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 15791
LENGTH: 274
TYPE: PRT
                                                                                                                                                                                                                                                                            MBER: US/09/610,906
2000-07-06
                                                                                                                                                                                                                                                                                                             09/226,994
                                                                                                                                              Sequence 12, Application US/09610906
Patent No. 6566066
GENERAL INFORMATION:
APPLICANT: Walker, Michael G.
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57.18;
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; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank
; PUBLICATION INFORMATION:
US-09-610-906-12
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                                                                210 GYWEPAW
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US-09-610-906-12
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GENERAL INFORMATION:
APPLICANT: Abbort Laboratories
APPLICANT: Mukerli, Pradip
APPLICANT: Mukerli, Pradip
APPLICANT: Huang, Yung-Sheng
APPLICANT: Huang, Yung-Sheng
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Thurmond, Jennifer M.
APPLICANT: Thurmond, Jennifer M.
APPLICANT: Toolard, Jennifer M.
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Toolard, Jennifer M.
FILE REFERENCE: 6407.US.P2
CURRENT APPLICATION NUMBER: US 09/379,095
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 278
TYPE: PRT
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Query Match Best Local Similarity 57.1%; Matches 4; Conservative 2, 2006, 08:58:26

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RESULT 2
US-10-437-963-176036
is Sequence 176036, Application US/10437963
is Publication No. US20040123343A1
is GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof
CURRENT APPLICATION NUMBER: US/10/437,963
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49513, A
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US-10-437-963-176036
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US-10-282-122A-52805
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US-10-425-115-287762
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US-10-425-115-344695

US-10-450-763-43035

US-10-450-761-9632

US-10-369-493-19811

US-10-450-022-7

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Pred. No. 1.3e
0; Mismatches
                                                                                                                                                              Sequence 30836, Application US/10425115
; Sequence 308836, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules an
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; TITLE OF SEQ ID NOS: 369326
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; LENGTH: 58
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  5-115-308836
  TYPE: PRT
ORGANISM: Zea 1
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APPLICANT: Yamamoto, Robert
APPLICANT: Yorsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential GerelLE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
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                                                                                                                                      Score 34; DB 4; L. Pred. No. 1.5e+02; ); Mismatches 3;
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Publication No. US20030170782A1

GENERAL INFORMATION:

APPLICANT: Microbial Technics limited

APPLICANT: Le Page, Richard W F

APPLICANT: Hanniffy, Sean B

TITLE OF INVENTION: Proteins

FILE REFERENCE: PWC/P21978WO

CURRENT APPLICATION NUMBER: US/10/091,007

CURRENT FILING DATE: 2002-03-06

PRIOR APPLICATION NUMBER: GB 9921125.2

PRIOR FILING DATE: 1999-09-07

NUMBER OF SEQ ID NOS: 276

SOFTWARE: Patentin version 3.0
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Pred. No. 6
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ilarity 57.1%;
Conservative
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Malone, Cheryl
Haselbeck, Robert
                                                                                                                                     Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
    204966
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                                                               Oryza sativa
NUMBER OF SEQ ID NOS:
SEQ ID NO 176036
LENGTH: 72
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Best Local Similarity
Matches 4; Conser
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US-10-282-122A-49513
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TH: 452
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                TYPE: PRT ORGANISM:
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US-10-369-493-23291

Sequence 23291, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION NUMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 23291

LENGTH: 469
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6.6e+02;
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Mismatches
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Pred. No.
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PRIOR FILING DAIE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
SEMAINING PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removing Prior Application data
SEQ ID NO 49513
LENGTH: 466
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US-10-282-122A-66258
; Sequence 66258, Application US/10282122A
; Publication No. US20040029129A1
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US-10-369-493-23291
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4; Conserv
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Best Local Similarity
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US/10/282,122A

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APPLICATION NUMBER:
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PLILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR PILING DATE: 2000-05-26

PRIOR PLILING DATE: 2000-05-26

PRIOR PLILING DATE: 2000-05-26

PRIOR PLILING DATE: 2000-09-06

PRIOR PLILING DATE: 2000-09-06

PRIOR PLILING DATE: 2000-09-06

PRIOR PLILING DATE: 2000-09-06

PRIOR PLILING DATE: 2000-10-23

PRIOR PLILING DATE: 2000-10-23

PRIOR PPLICATION NUMBER: 60/242,578

PRIOR PLILING DATE: 2000-10-23

PRIOR PPLICATION NUMBER: 60/267,636

PRIOR PLING DATE: 2000-12-22

PRIOR PPLING DATE: 2000-12-22

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2001-12-22

PRIOR PLILING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16
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ILE REFERENCE: ELITRA.034A
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Sequence 52805, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66258
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Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Wang, Liangsu
Zamudio, Carlos
Malone, Cheryl
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Best Local Similarity 57.1
Matches 4; Conservative
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US-10-282-122A-52805
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 13733
LENGTH: 475
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Pred. No. 6.7e+02;
); Mismatches 3;
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Mismatches 3
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Pred. No.
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         PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
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; Sequence 13733, Application US/10369493
; Publication No. US20030233675A1
3-02-20
60/191,078
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2000-11-27
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Conservative
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illarity 57.1%;
Conservative
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APPLICATION NUMBER: 60/2
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SOFTWARE: PatentIn ver
SEQ ID NO 52805
LENGTH: 474
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Best Local Similarity
Matches 4; Conser
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APPLICANT: Cao, Yon
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                                                              Genes
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Pred. No. 6.7e+02;
; Mismatches 3
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                                                                Essential
                                                                                                   MBER: US/10/282,122A
2003-02-20
ER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ication data removed
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                                                                                                                CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
                                                         TITLE OF INVENTION: Identification of FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,
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ILING DATE: 2000-05-26
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Yamamoto, Robert
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US-10-282-122A-68169
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    Robert
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lio, Carlos
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Trawick, John
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APPLICATION NUMBER: FILING DATE: 2001-0.
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Haselbeck, Ro
Ohlsen, Kari
Zyskind, Judi
Wall, Daniel
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NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn vers
SEQ ID NO 68169
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CURRENT APPLICAT
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Best Local S
Matches 4
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Pred. No. 6.7e+02;
0; Mismatches 3;
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APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essenti:
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A .
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-28
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-09
SSULT 9
S-10-282-122A-57680
Sequence 57680, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
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; Sequence 68169, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
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Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
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Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
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Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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SOFTWARE:
SEQ ID NO
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APPLICANT: Kubo, Hajime

; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS

; FILE REFERENCE: 28967/37084A

; CURRENT APPLICATION NUMBER: US/10/046,922

; CURRENT FILING DATE: 2002-01-15

; NUMBER OF SEQ ID NOS: 80

; SOFTWARE: Patentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 585;
                                                                                                                                                                         APPLICANT: Newman, Mark
APPLICANT: Brown, David
TITLE OF INVENTION: Methods and System for Optimizing Multi
TITLE OF INVENTION: Acid Constructs and Peptides Encoded T
FILE REFERENCE: 2060.0320004
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Pred. No. 7.9e+02;
); Mismatches 3,
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47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33;
Pred. No.
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                                 Sequence 87, Application US/10474960A
Publication No. US20040248113A1
GENERAL INFORMATION:
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Publication No. US20020164667A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
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SOFTWARE: FastSEQ for Windows
                                                                                              Sette, Alessandro
Chesnut, Robert
Livingston, Brian
Baker, Denise
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OTHER INFORMATION: X
NAME/KEY: SITE
LOCATION: (10)..(10)
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    RESULT 13
US-10-474-960A-87
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US-10-046-922-34
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TH: 585
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LENGTH: 10
                                        Sequence 87,
Publication
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Sequence 87, Application US/09894018

Patent No. US20020119127A1

GENERAL INFORMATION:

APPLICANT: Sette, Alessandro

APPLICANT: Chestnut, Robert

APPLICANT: Livingston, Brian

APPLICANT: Baker, Denisw

APPLICANT: Baker, Denisw

APPLICANT: Brown, David

TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY

FILE REFERENCE: 39963-20033.00

CURRENT APPLICATION NUMBER: US/09/894,018

CURRENT PILING DATE: 2001-06-27

PRIOR APPLICATION NUMBER: US 60/173,390

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 2001-04-16

NUMBER OF SEQ ID NOS: 368

SOFTWARE: FastSEQ for Windows Version 4.0

SEO TD NO 87
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Pred. No. 7e+02;
); Mismatches
                                                                                                                                                                                                                                                             See
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-09
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ORGANISM: Artificial Sequence
FEATURE:
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US-10-282-122A-50338
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US-10-046-922-35
; Sequence 35, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PATENTIN VERSION 3.0
; SEQ ID NO 35
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
US-10-046-922-35
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 10;
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Pred. No. 47;
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Matches 4; Conservative
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US-11-087-099-1003

US-11-087-099-1003; Application US/11087099; Publication No. US20060041961A1; GENERAL INFORMATION:

TITLE OF INVENTION: Genes and Uses for F; FILE REFERENCE: 38-21(53450)B EP; CURRENT APPLICATION NUMBER: US/11/087,09; CURRENT FILING DATE: 2005-03-22; NUMBER OF SEQ ID NOS: 12464; SEQ ID NO 1003; LENGTH: 464
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                      Sequence 968, App Sequence 5906, Ap Sequence 10025, Ap Sequence 10025, Ap Sequence 1117, Ap Sequence 1117, Ap Sequence 7125, Ap Sequence 7125, Ap Sequence 12720, Ap Sequence 1275, Ap Sequence 262, App Sequence 262, App Sequence 262, App Sequence 262, App Sequence 263, App Sequence 263, App Sequence 263, App Sequence 261, Ap Sequence 263, App Sequence 263, App Sequence 263, App Sequence 261, Ap Sequence 25130, Ap Sequence 2130, Ap Sequence 2130, Ap Sequence 2130, Ap
                    US-10-995-561-968

US-11-079-463-8428

US-11-079-463-7586

US-11-079-463-10025

US-11-079-463-10025

US-11-129-741-3641

US-10-929-988-81

US-10-821-234-1610

US-10-821-234-1610

US-10-821-234-1610

US-11-087-099-7125

US-11-045-024-4377

US-11-045-024-4501

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US-11-087-099-11321
; Sequence 11321, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for P)
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099;
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 11321
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Mismatches 3
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US-11-087-099-7571

Sequence 7571, Application US/11087099

Publication No. US20060041961A1

GENERAL INFORMATION:

APPLICANT: Abad, Mark S. et al.

TITLE OF INVENTION: Genes and Uses for Plant

FILE REFERENCE: 38-21(53450)B EP

CURRENT APPLICATION NUMBER: US/11/087,099

CURRENT FILING DATE: 2005-03-22

NUMBER OF SEQ ID NOS: 12464

SEQ ID NO 7571

LENGTH: 475
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Pred. No. 9
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Pred. No.
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US-11-087-099-2298; Application US/11087099; Sequence 2298, Application US/11087099; Publication No. US20060041961A1; GENERAL INFORMATION:
TITLE OF INVENTION: Genes and Uses for FILE REFERENCE: 38-21(53450)B EP; CURRENT APPLICATION NUMBER: US/11/087,09; CURRENT FILING DATE: 2005-03-22; NUMBER OF SEQ ID NOS: 12464; SEQ ID NO 2298; LENGTH: 475
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; Sequence 6764, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Pseudomonas putida KT2440
US-11-087-099-2298
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             ; LENGTH: 475
; TYPE: PRT
; ORGANISM: Pseudomonas syringae pv.
US-11-087-099-1870
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SEQ ID NO 1870
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Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(53450)B EP CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 12291
LENGTH: 472
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Sequence 1870, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
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Pred. No. 91; ; Mismatches
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US-11-188-298-19864, Application US/11188298

Publication No. US20060075522A1

GENERAL INFORMATION:

TITLE OF INVENTION: GENES AND USES FOR PLANT

FILE REFERENCE: 38-21(53452)B

CURRENT APPLICATION NUMBER: US/11/188,298

CURRENT FILING DATE: 2005-07-22

PRIOR APPLICATION NUMBER: 60/592,978

PRIOR FILING DATE: 2004-07-31

NUMBER OF SEQ ID NOS: 22569

SEQ ID NO 19864

LENGTH: 471
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Pred. No. 9
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Pred. No.
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TITLE OF INVENTION: Genes and Uses for Plant FILE REFERENCE: 38-21(53450)B EP CURRENT APPLICATION NUMBER: US/11/087,099 CURRENT FILING DATE: 2005-03-22 NUMBER OF SEQ ID NOS: 12464 SEQ ID NO 1256 LENGTH: 476
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Mismatches
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US-11-087-099-7019

Sequence 7019, Application US/11087099

Publication No. US20060041961A1

GENERAL INFORMATION:

APPLICANT: Abad, Mark S. et al.

TITLE OF INVENTION: Genes and Uses for Plant

FILE REFERENCE: 38-21(53450)B EP

CURRENT APPLICATION NUMBER: US/11/087,099

CURRENT FILING DATE: 2005-03-22
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ritle of invention: Genes and USES FOR PLANT; File Reference: 38-21(53452)B
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR FILING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 6764
LENGTH: 475
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Pred. No.
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Pred. No. 9
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Pred. No.
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; Sequence 1256, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
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US-11-087-099-1256 .
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SEQ ID NO 7019
LENGTH: 478
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US-11-087-099-7019
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US-11-188-298-6764
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Sequence 4146, Application US/11087099;
publication No. US20060041961A1;
GENERAL INFORMATION:
TITLE OF INVENTION: Genes and Uses for Plant Improvement;
FILE REFERENCE: 38-21(53450)B EP;
CURRENT APPLICATION NUMBER: US/11/087,099;
CURRENT FILING DATE: 2005-03-22;
NUMBER OF SEQ ID NOS: 12464;
SEQ ID NO 4146;
LENGTH: 482
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US-11-188-298-8872, Application US/11188298
; Sequence 8872, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; TITLE OF INVENTION:
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT;
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 8872
; LENGTH: 478
RESULT 11
US-11-087-099-9555
US-11-087-099-9555
Sequence 9555, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 9555
LENGTH: 478
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Pred. No. 92;
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US-11-087-099-9555
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US-11-087-099-4146
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103 GYWFAYW 109

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Search completed: May
Job time: 9.93023 secs
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APPLICANT: ITO, MIKITO
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: KAWADA, YOKO
APPLICANT: KAWADA, YOKO
APPLICANT: SHIBUYA, MASABUMI
TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
FILE REFERENCE: 249-107
CURRENT APPLICATION NUMBER: US/09/453,718
PRIOR APPLICATION NUMBER: US/09/453,718
PRIOR PILING DATE: 1999-12-03
PRIOR PILING DATE: 1999-05-20
PRIOR PILING DATE: 1998-07-20
PRIOR FILING DATE: 1998-07-20
PRIOR FILING DATE: 1998-07-20
PRIOR PILING DATE: 1998-07-20
PRIOR PILING DATE: 1998-07-20
PRIOR PILING DATE: 1998-07-20
PRIOR PILING DATE: 1997-11-21
SOFTWARE: PATENTING VOICE: 2.1
SEQ ID NO 97
LENGTH: 119
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US-11-087-099-9097
; Sequence 9097, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9097
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens PfO-1
US-11-087-099-9097
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0; Mismatches
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Mismatches
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Pred. No. 9
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S-11-250-411-97
Sequence 97, Application US/11250411
Publication No. US20060034838A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
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-68 US-10-046-922-035 score: Title: Perfect

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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# ALIGNMENTS

Rhesus D antibody binding peptide; Rhesus D; RhD; identification; anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy; prophylaxis; haemolytic disease of the newborn; HDN; ITP; idiopathic thrombocytopaenic purpura; immunoglobulin. antibody binding peptide SEQ ID NO:4. AAB99759 standard; peptide; 10 AA entry) (first 21-SEP-2001 AAB99759; Ω Rhesus RESULT 1 AAB99759 

99EP-00122858 EP1106625-A1. 17-NOV-1999; 13-JUN-2001. Homo 

Fisch Hofmann A, Miescher S,

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99EP-00122858.

17-NOV-1999;

BIOPLASMA AG

(ZLBB-) ZLB

2001-383568/41 WPI;

the of Novel peptides capable of binding Rhesus D antibodies are used to manufacture an agent for the diagnosis, therapy or prophylaxis of diseases associated with Rhesus D antigen, e.g. hemolytic disease newborn (HDN).

12; 19pp; English. Page ٦; Claim

more The present sequence represents a peptide capable of binding Rhesus D antibodies (I). Also described in the present invention are: (1) a nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more (II) operably linked to an expression control system; (3) a cell (IV) comprising (II) or (III); (4) preparing (I); (5) identifying (M1) peptides having immunologic properties of Rhesus D protein epitopes comprising subjecting an antibody/antibody fragment recognising an epitope of Rhesus D protein to several panning rounds with a phage display library, and identifying immunogenic peptide sequences which are

ase of the is used to of antibodies purified tions. Using (I) as using immunisation the amino acid immunological ssion of mimotopes which differ in their amino acid sequence from the amino ac sequences of Rhesus D protein; and (6) peptides (V) with immunologics properties of Rhesus D protein epitopes obtained by (M1). (I) is used manufacture an agent for the diagnosis, therapy or prophylaxis of diseases associated with Rhesus D antigen, e.g. haemolytic disease of newborn (HDN) or idiopathic thrombocytopaenic purpura (ITP), for the manufacture of an affinity reagent for anti-Rhesus D antibodies purif or removed from body fluids or immunoglobulin preparations. Using (I) an immunogen to raise anti-Rhesus D antibodies avoids using immunisat with foreign erythrocytes thereby avoiding the risk of transmission o viral diseases like AIDS and hepatitis B Gaps ö Length 10 Indels 3, 4, DB 12; Mismatches Score 34; Pred. No. ö 97.1%; 57.1%; Conservative Similarity Sequence 10 AA; 4. Query Match Best Local S Matches 4 

7 7 GYWSAKW GYWXXXW g ò

standard; peptide; AAB99769 AAB99769

**AAB99769** 

entry) (first 21-SEP-2001

**₩** antibody related peptide Ω Rhesus

RhD; identification; ö Rhesus D antibody binding peptide; Rhesus D; RhD; identificatio anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy; prophylaxis; haemolytic disease of the newborn; HDN; ITP; cycliidiopathic thrombocytopaenic purpura; immunoglobulin; circular.

Homo sapiens Synthetic.

Location/Qualifiers 1. .12 Disulfide-bond

EP1106625-A1

13-JUN-2001

99EP-00122858 17-NOV-1999;

99EP-00122858 17-NOV-1999;

ZLB BIOPLASMA AG (ZLBB-)

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2001-383568/41 WPI;

the oŧ to of se Novel peptides capable of binding Rhesus D antibodies are used manufacture an agent for the diagnosis, therapy or prophylaxis diseases associated with Rhesus D antigen, e.g. hemolytic diseasesnewborn (HDN).

Example 1; Page 8; 19pp; English.

more e or (IV) The present invention describes peptides capable of binding Rhesus D antibodies (I). Also described in the present invention are: (1) a nucleic acid (II) encoding (I); (2) a vector (III) comprising one or (II) operably linked to an expression control system; (3) a cell (IV) comprising (II) or (III); (4) preparing (I); (5) identifying (M1) peptides having immunologic properties of Rhesus D protein epitopes comprising subjecting an antibody/antibody fragment recognising an epitope of Rhesus D protein to several panning rounds with a phage 

display library, and identifying immunogenic peptide sequences which are mimotopes which differ in their amino acid sequence from the amino acid sequences of Rhesus D protein; and (6) peptides (V) with immunological properties of Rhesus D protein epitopes obtained by (M1). (I) is used to manufacture an agent for the diagnosis, therapy or prophylaxis of elementacture an agent for the diagnosis, therapy or prophylaxis of the newborn (HDN) or idiopathic thrombocytopaenic purpura (ITP), for the manufacture of an affinity reagent for anti-Rhesus D antibodies purified or removed from body fluids or immunoglobulin preparations. Using (I) as an immunogen to raise anti-Rhesus D antibodies avoids using immunisation with foreign erythrocytes thereby avoiding the risk of transmission of viral diseases like AIDS and hepatitis B. The present sequence represents an anti-Rhesus D (RhD) antibody related peptide which is used in an example from the present invention 

Sequence 12 AA;

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·. Gaps .. 0 Length 12; Indels т М 4 ore 34; DB ed. No. 14; Mismatches Score 34; Pred. No. ·. 97.1%; 57.1%; Conservative Query Matcn Best Local Similarity 4. Matches

GYWSAKW GYWXXXW Н ~

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AAU03644 standard; protein; AAU03644

452 entry) (first 12-SEP-2001 AAU03644;

antigenic protein, ID-119 Streptococcus m Group

sepsis; tract; Group B Streptococcus; encapsulated bacterium; therapeutic; meningitis; neonate; antigenic; vaccine; infection; genital capsid polysaccharide vaccination.

Streptococcus agalactiae

WO200132882-A2. 

10-MAY-2001

2000WO-GB003437. 07-SEP-2000;

99GB-00021125. 07-SEP-1999; (MICR-) MICROBIAL TECHNICS LTD

Hanniffy Wells JM, RWF, Page Гe

SB

WPI; 2001-31644/33 N-PSDB; AAS07061.

New polypeptides derived from Streptococcus agalactiae are useful to provide detection of, and vaccination against, Group B Streptococcus infections, particularly to prevent infection in neonatals.

Fig 1; 178pp; English Claim 1;

AAU03601-AAU03722 represent Group B Streptococcus (Streptococcus agalactiae) amino acid sequences of the invention. S. agalactiae is an encapsulated bacterium which is a major pathogen of humans causing sepsis and meningitis in neonates as well as adults. The S. agalactiae antigenic polypeptides are used to vaccinate against Group B Streptococcus infections, particularly to prevent infection in new born children arising from the maternal genital tract. An immunogenic composition is useful in the preparation of a medicament for the treatment or prophylaxis of Group B Streptococcus infection. The invention does not have the disadvantages of varied response rate associated with prior art

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the 6213 antisense sequences given in the specification where expression the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated on the polypeptide or its fragment whose expression is inhibited by the antisense contingense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or the biological or a gene on which the test compound that inhibits proliferation of an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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polysaccharide vaccination
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2001US-00948993.
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25-OCT-2001;
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strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant is a crop plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
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cuch as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties.

The recombinant DNA construct is useful for improving plant properties.

The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.html.
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Sequence 469 AA;

Gaps . 0 Indels Length Score 34; DB 8; Le Pred. No. 4.6e+02; ; Mismatches 3; ;; 0 97.1%; ilarity 57.1%; Conservative Similarity 4; Conserv Query Match Best Local S Matches 4

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7 GYWXXXW -1

103 GYWVASW 97

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standard; protein; ABU38334 RESULT **ABU383** 

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entry) (first 9-JUN-2003 ABU38334;

gene Protein encoded by Prokaryotic essential design

Antisense; prokaryotic essential gene; cell proliferation; drug

aeruginosa Pseudomonas

WO200277183-A2

03-OCT-2002

2002WO-US009107 21-MAR-2002; 2001US-00815242. 2001US-00948993. 2001US-0342923P. 2002US-00072851. 2002US-0362699P. 21-MAR-2001; 06-SEP-2001; 25-OCT-2001; 08-FEB-2002; 06-MAR-2002;

INC PHARM ELITRA (ELIT-)

WPI; 2003-029926/02 N-PSDB; ACA42204. 

SEQ ID NO 66258; 1766pp; English. Claim 25;

for

candidate molecules

solate

antisense nucleic acids, homologous nucleic acids

Nek for Zyskind .Xu HH;

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Ohlsen Forsyth

Haselbeck 'R Yamamoto R,

ບັ GJ,

Malone Carr G

c, JD,

Zamudio ( Trawick

Wang L, Wall D,

WPI; 2003-029926/02 N-PSDB; ACA28751.

ELITRA PHARM INC

(ELIT-)

screening

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useful for identifying proteins or srequired for cellular proliferation for rational drug discovery programs.

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Zyskind Xu HH;

Ohlsen Forsyth

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Haselbeck R Yamamoto R,

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Wang Wall

expression one any The invention relates to an isolated nucleic acid comprising an the 6213 antisense sequences given in the specification where e of the nucleic acid inhibits proliferation of a cell. Also incl

cucleic acid, (2) a host cell containing the vector; (3) an isolated nucleic acid, (2) a host cell containing the vector; (3) an isolated public acid, (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway required for proliferation, or that inhibites cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product is gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) proliferation of an organism acts; (9) manufacturing an antibiotic; (10) prolifing a compound's activity; (11) a culture comprising strains in which the spen product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for proliferation to isolate candidate molecules for rational for cellular proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target processing jenes in the present sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ; 0 design drug .. 0 gene; cell proliferation; Length 472; Indels essential gene #10408. Score 34; DB 6; Le Pred. No. 4.6e+02; ; Mismatches 3; ABU24881 standard; protein; 474 AA Antisense; prokaryotic essential ; 0 Prokaryotic 2001US-00815242. 2001US-00948993. 2001US-0342923P. 2002US-00072851. 2002US-0362699P. 2002WO-US009107 97.1%; entry) Conservative Clostridium botulinum 100 (first encoded by 7 Query Match Best Local Similarity GYWISAW GYWXXXW Sequence 472 AA; WO200277183-A2 21-MAR-2001; 06-SEP-2001; 25-OCT-2001; 08-FEB-2002; 06-MAR-2002; 21-MAR-2002; 19-JUN-2003 03-OCT-2002 4 ; 94 Н ABU24881 Protein Best Loc Matches RESULT 7 ABU24881 g ð

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide, (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of agene in an operon required for proliferation or the activity of enclosed or that influences the activity of identifying a compound that influences the activity of equipment of the proliferation, or that inhibits cellular proliferation; (8) identifying a gene required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound,'s activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent proliferation of an organism, or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for for erlular proliferation to an organism. The antisense nucleic acids required for erlular proliferation of an organism. The antisense molecules for rational and also accenting for homologous nucleic acids required the acids and action of an organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhin K. pneumoniae or P. aeruginosa. The present sequence is encoded by the target prokaryotic essential genes. Note: The sequence data for patent did not form part of the printed specification, but was obtain electronic format directly from WIPO at
          New antisense nucleic acids, useful for identifying proteins or tor homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus; GAS; GBS; group B streptococcus; Streptococcus group A streptococcus; Streptococcus pyogenes; antibacterial; antinfammatory; infection; vaccine; meningitis; gene therap
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Pred. No. 4.6e+02;
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                                                                                            52805; 1766pp; English
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57.1%;
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in a cativity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and activity. (I), nucleic acids encoding (I), are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. (I) sused to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to recombinantly produce (I) and may be acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
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                                                                                                                                                        infection
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                                                                                                                                                     New Streptococcus protein for the treatment or prevention of disease caused by Streptococcus bacteria, such as meningitis, detecting a compound that binds to the protein.
                                                                            Fraser
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2001US-00948993.
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24-NOV-2000; 2000GB-00028727
07-MAR-2001; 2001GB-00005640
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INST GENOMIC
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N-PSDB; ABN71191.
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25-OCT-2001;
08-FEB-2002;
06-MAR-2002;
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ABU40245
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of agene in an operon required for proliferation, or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required gene or its gene product lies or agene on which the test compound that inhibits proliferation of an compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of the strains is present in a culture or collection of the strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for a compound received or rational drug discovery programs or for arreaning for homologous nucleic acids required for a continue or cellular proliferation of an organism or for arreaning for homologous nucleic acids required for a continue or cellular proliferation of an organism or for arreaning for monologues or acids required for a continue or cellular proliferation or for arreaning for monologues.
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Xu HH;
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                                                                                                                                             New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs
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                                Ohlsen Porsyth
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4.6e+02;
3;
                                   Haselbeck R,
Yamamoto R,
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                                                                                                                                                                                                                         SEQ ID NO 68169; 1766pp; English,
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Pred. No.
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larity 57.1%;
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N-PSDB; ACA44115.
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                                                                                                                                                                                                                      Claim 25;
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The invention relates to an isolated nucleic acid comprising any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid cencoding a polypeptide whose expression is inhibited by the antisense conclude or its fragment whose expression is inhibited by the antisense conclude or its fragment whose expression is inhibited by the antisense conclude or its fragment whose expression is inhibited by the antisense nucleic acid, (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of agene in an operon required for the activity of agene in an operon required for proliferation, or that inhibites cellular proliferation; (7) identifying a gene frequired gene or its gene product lies or a gene or which a proliferation or the biological identifying a gene required for cellular proliferation or the biological corporation, or that inhibites proliferation of an organism acts, (9) manufacturing an antibiotic, (10) profilling a compound's activity, (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound that inhibite proliferation of an organism. The antisense nucleic acids are useful for strains; or (13) identifying the target of a compound that inhibite the corpoliferation of an organism. The antisense nucleic acids are useful for cellular proliferation in cells other than S. aureus, S. typhimurium, chard discovery programs, or for screening for homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, charent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                       useful for identifying proteins or screening required for cellular proliferation to for rational drug discovery programs.
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Forsyth
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Pred. No. 4.6e+02;
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Yamamoto R
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                            2001US-00815242.
2001US-00948993.
2001US-0342923P.
2002US-00072851.
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for homologous nucleic acids
isolate candidate molecules f
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ilarity 57.1%;
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06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
06-MAR-2002;
21-MAR-2002;
                                                                                                                                                                                                                                                                                                                          Claim 25;
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SEO ID

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agalactiae protein

Streptococcus

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24-FEB-2005

ADV87906;

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standard;

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4DV87906

infection

Antibacterial; Vaccine; bacterial

agalactiae

Streptococcus

FR2824074-A1

31-OCT-2002

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transformed plant, where the polymelectide or polypeptide is useful for improving plant properties.

The recombinant DNA construct is useful for improving plants with improved plant properties, e.g. improved cold, heat or aforought tolerance, improved plant properties, extreme osmotic conditions, pathogens or pests, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved plant growth and development under at least one stress condition, improved lignin production of photosynthesis or by providing improved lignin production or improved galactomannan contition, improved lignin production or improved galactomannan contition, improved lignin production or improved galactomannan production. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NA construct comprising a promoter positioned to prova
a polynucleotide encoding a polypeptide from a
useful for producing plants with improved properties
                                          kecombinant DNA construct; transformed plant; improved plant | cold tolerance; heat tolerance; drought tolerance; herbicide; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbonitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
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                                 polypeptide
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02-DEC-2004
                                  Bacterial
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Frangeul L, Lalioui Poyart C, Trieu CP,

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26-APR-2001; 2001FR-00005642.

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26-APR-2001;

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Glaser Zouine WPI; 2004-101891/11

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The present invention relates to novel Streptococcus agalactiae

nucleotide sequences (I; ADV87607-ADV87745) and novel polypeptides of S.
ADV87746-ADV89950). The nucleotide sequences encode polypeptides of S.
agalactiae involved in the synthesis of amino acids, cell membranes,
intermediate (central) metabolism, energetic metabolism, fatty acid and
phospholipid metabolism, nucleotide metabolism including purines,
pyrimidines and/or nucleosides, regulatory functions, replication,
transcription, translation, protein transport, adaptation to atypical
conditions, sensitivity to medicines and/or analogues, functions related
to transposons, biosynthesis of cofactors, prosthetic groups and
transporters, cell membrane proteins and cellular machinery. (I) are
useful for the detection and/or amplification of nucleic acids.
Pharmaceutical composition comprising (I) or (II) are useful for
treatment of a bacterial S. agalactiae infection. Note: WO200292818A2
contains 6617 sequence whereas the present patent only contains 2344
                                                                                                                                                                                                                                                                                                                                                                                                                            related
                                                                                                                                                                                                Genomic nucleotide sequences encoding polypeptides of Streptococcus agalactiae for the development of vaccines, diagnostic tools, DNA chips and identification of therapeutic targets.
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Pred. No. 4.6e+02
; Mismatches
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ilarity 57.1%;
Conservative
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ilarity 57.1%;
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                                                                                  26-APR-2001; 2001FR-00005642
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Couve E,
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                                              26-APR-2002;
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14-MAY-1998
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Zouine M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to novel Streptococcus agalactiae

nucleotide sequences (I; ADV78860-ADV7898 and ADV81205-ADV85476) and
novel polypeptides (II; ADV78999-ADV81203 and ADV81205-ADV83340). The
nucleotide sequences encode polypeptides of S. agalactiae involved in the
synthesis of amino acids, cell membranes, intermediate (central)
metabolism, energetic metabolism, fatty acid and phospholipid metabolism,
nucleotide metabolism including purines, pyrimidines and/or nucleosides,
regulatory functions, replication, transcription, translation, protein
transport, adaptation to atypical conditions, sensitivity to medicines
and/or analogues, functions related to transposons, biosynthesis of
cofactors, prosthetic groups and transporters, cell membrane proteins and
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ne complete
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Poyart C, Trieu-Cuot
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Pred. No. 4.6e+02;
); Mismatches 3;
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                                                  infection
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                  SEQ ID
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                                                  Antibacterial; vaccine; bacterial
                   Streptococcus agalactiae protein,
                                                                                                                                                                                                                                                                                                            Chevalier
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Buchrieser
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                                                                                                                                                                                                                                                                                                            Rusniok (
Couve E,
                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-101891/11
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The present invention relates to novel Streptococcus agalactiae

nucleotide sequences (I; ADV78860-ADV78998 and ADV83341-ADV85476) and
novel polypeptides (II; ADV78999-ADV81203 and ADV81205-ADV83340). The
nucleotide sequences encode polypeptides of S. agalactiae involved in the
synthesis of amino acids, cell membranes, intermediate (central)
metabolism, energetic metabolism, fatty acid and phospholipid metabolism,
concleotide metabolism including purines, pyrimidines and/or nucleosides,
regulatory functions, replication, transcription, translation, protein
cand/or analogues, functions related to transposons, biosynthesis of
coffactors, prosthetic groups and transporters, cell membrane proteins and
cellular machinery. (I) are useful for the detection and/or amplification
of nucleic acids. Pharmaceutical composition comprising (I) or (II) are
useful for treatment of a bacterial S. agalactiae infection. The complete
genome of Streptococcus agalactiae is given in ADV81204. Note: The
present patent is an equivalent for the basic patent FR2824074A1, which
contains only 2344 sequences.
                                                                                                                                                                                    Genomic nucleotide sequences encoding polypeptides of Streptococcus agalactiae for the development of vaccines, diagnostic tools, DNA chips and identification of therapeutic targets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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    Frangeul L, Lalioui
Poyart C, Trieu-Cuot
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                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide one of 10 fully defined sequences given in the (or comprising 40 sequential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and single-stranded probe comprising the nucleic acid. The nucleic acids is useful for diagnosing pathological conditions regulting from E. faecium bacterial infection (e.g. urinary tract infection) and for screening drugs such as agonists and antagonist nucleic acid is useful for recombinant production of Candida albic derived peptides or antisense polypeptides. Pharmaceutical compositand vaccines containing the nucleic acid are useful for preventing treating Enterococcus faecium infections. The présent sequence reptone if the disclosed E. faecium proteins.
                                                                                                                                          New isolated nucleic acid derived from Enterococcus faecium end
Enterococcus faecium polypeptide useful for detection, preventi
treatment of a pathological condition resulting from a bacteria
infection.
                                                                                                                                                                                                                                             Example 1; SEQ ID NO 6868; 243pp; English.
                CORP
             THERAPEUTICS
                                                      Bush D;
                                                                                         WPI; 2003-799836/75
N-PSDB; ADC93587.
                                                      Doucette-Stamm LA,
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                 (GENO-) GENOME
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. 0 Length 478; Indels Score 34; DB 7; Le Pred. No. 4.7e+02; ); Mismatches 3; . 0 Query Match Best Local Similarity 57.1%; Matches 4; Conservative GYWXXXW <del>, ,</del> င်

98 GYWLSAW 104 g

2, 2006, 08:54:54 Search completed: May Job time: 93,2326 secs Н

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Biocceleration Ltd
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sw model using protein search, OM protein 08:47:12 2, 2006, May Run on:

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US-10-046-922-68 35 æ 1 GYWXXXWX score Sequence: Title: Perfect

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residues 96216763 seds, 283416 Searched 283416 of hits satisfying chosen parameters: Total number

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#### SUMMARIES

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# ALIGNMENTS

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TO3190
hypothetical protein 72B - rice mitochondrion
C;Species: mitochondrion Oryza sativa (rice)
C;Species: mitochondrion Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03190
R;Itadani, H.; Wakasugi, T.; Sugita, M.; Sugiura, M.; Nakazono, M.; Hirai, A.
Plant Call Physiol. 35, 1239-1244, 1994
A;Title: Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA: the exis A;Reference number: 214841; MUID:95211382; PMID:7545979
A;Accession: T03190
A;Reference number: 214841; MUID:95211382; PMID:7545979
A;Accession: T03190
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cossidues: 1-72 <ITA>
A;Cossidues: 1-72 <ITA>
A;Coss-references: UNIPROT:035302; UNIPARC:UPI00009746F; EMBL:D32052; NID:9769704;
A;Experimental source: cultivar Nipponbare
C;Genetics:
A;Genome: mitochondrion
C;Keywords: mitochondrion
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#text\_change 09-Jul-2004 Thiobacillus ferrooxidans plasmid pTF1

a Thiobacillus ferrooxidan EMBL: X52699; NID: 94.8158; S12193
S12193
hypothetical protein 4 - Thiobacillus ferrooxidans plasmid pTF:
C;Species: Thiobacillus ferrooxidans
C;Species: Thiobacillus ferrooxidans
C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_chang(C;Accession: S12193
R;Drolet, M.; Zanga, P.; Lau, P.C.K.
Mol. Microbiol. 4, 1381-1391, 1990
A;Title: The mobilization and origin of transfer regions of a A;Title: The mobilization and origin of transfer regions of a A;Title: The mobilization and origin of transfer regions of a A;Reference number: S12188; MUID:91125140; PMID:2280689
A;Reference number: S12193
A;Accession: S12193
A;Accession: S12193
A;Accession: UNIPROT:P20088; UNIPARC:UPI000013B9EC; EMB
A;Genome: plasmid pTF1

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A.; Larbig,
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
C;Accession: E83497
R;Stover, C.K.; Pham, X.O.: Frwin T
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Nature 406, 959-964, 2000

A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A; Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: E83497
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-472 <STO>
A; Cross-references: UNIPROT: Q914E4; UNIPARC: UPI00000C529E;
A; Experimental source: strain PAO1
C; Genetics:
A; Gene: PAl194
C; Superfamily: ecotropic retrovirus receptor protein
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L.L.; Coulter,
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S.; Hullo, M.F.
, A.; Lardinois,
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Portetelle
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.; Carter, N.M.; Cho
et. C.; Ferrari, E.
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sato, V.; Uchiyama
ata, K.; Yoshida, I
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
C;Accession: D70048
R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, C; Bron, S; Bronillet', S; Bruschi, C.V.; Caldwell, B; Capuano, V; Carter, A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Fe Nature 390, 249-256, 1997, Emmerson, P.T.; Entian, M.D.; Frington, J.; Fabret, C.; Fe Nature 290, 249-256, 1997, M.; Hilbert, H.; Holsappel, S; Hosono, S; H Koetter, P; Koningstein, G; Krogh, S; Kumano, M; Kurita, K; Lapidus, A.; A; Authoros: Lauber, J.; Lazarevic, V; Lee, S.M.; Levine, A.; Liu, H; Nasuda, Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T. Y., Minters, P.; Wipat, A.; Tanakoa, T.; Terpstra, P.; Tognoni, A.; Tasako, V.; A, Authoros: Schleich, S.; Schroeter, P.; Yamanoco, H.; Yamano, K.; Yasumoto, K.; Yata, K.; Yakaubres: Yoshikawa, H.; Zunstein, B.; Yoshikawa, H.; Danchin, A.; Tosako, V.; A; Authoros: Yoshikawa, H.; Zunstein, B.; Yoshikawa, H.; Danchin, A.; Arcession: D7048
A; Reference number: A69580; MUID:98044033; PMID:9384377
A; Roseldues: Preliminary; nucleic acid sequence not show; translation not shown A; Roseriencia: Preliminary and Source: strain 168
A; Gomerics:
A; Genetics:
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phl, T.M.;
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                                                                                                                                            hypothetical protein SCJ9A.03c - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2 C; Accession: T37139

R; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M. submitted to the EMBL Data Library, August 1999

A; Reference number: Z21622

A; Reference number: Z21622

A; Reference number: Z21622

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Pred. No. 78;
0; Mismatches
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Pred. No. 59;
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(house mouse)
A; Residues: 1-497 <STO>
A; Cross-references: UNIPROT: Q9CE19; UNIPROT: Q0CE19; UNIPROT: Q0
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A; Residues: 1-490 <STO>
A; Cross-references: UNIPROT: Q9CE15; UNIPARC: UPI0000C6B99; GB: AE005176;
A; Experimental source: strain IL1403
C; Genetics:
A; Gene: arcD1
C; Superfamily: ecotropic retrovirus receptor protein
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 A; Molecule type: DNA
A; Residues: 1-482 <LUE>
A; Cross-references: UNIPROT:P18275; UNIPARC:UP100000618AA; GB:M33223; N; Experimental source: strain PAO1
A; Experimental source: strain PAO1
A; Note: the gene encoding this protein is located upstream of the arcAB R; Stover, C.K.; Pham, X.O.; Ewin, A.L.; Mizoguchi, S.D.; Warrener, P.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opple ference number: A82950; MUID:20437337; PMID:10984043
A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-482 <STO>
A; Residues: 1-482 <STO>
A; Cross-references: UNIPARC:UPI0000618AA; GB:AE004930; GB:AE004091; NI:A; Cross-references: Strain PAO1
C; Genetics:
A; Gene: arcD; PA5170
C; Superfamily: ecotropic retrovirus receptor protein
C; Keywords: transmembrane protein
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C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 05-C;Accession: G86878
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; W Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: G86878
A;Status: preliminary
A;Molecule type: DNA
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Mismatches
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Pred. No. 80
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Best Local Similarity 57.1%;
Matches 4; Conservative
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-490 <STC
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genome of the bacterium Mycoplasma pneumoni
PMID:8948633
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                                                                                                                                                                                                                                                   C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 1
C; Accession: C34903
R; Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A; Title: Active site structure and antigen binding properties of A; Reference number: A34903; MUID:90094387; PMID:2104617
A; Accession: C34903
A; Accession: C34903
A; Accession: C34903
A; Residues: 1-142 < BED>
A; Residues: 1-142 < BED>
A; Residues: 1-142 < BED>
A; Cross-references: UNIPARC:UPI0000176C0F
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-119/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase N;Alternate names: hypothetical protein A65_orf227 C;Species: Mycoplasma pneumoniae A;Variety: ATCC 29342 A;Variety: ATCC 29342 C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change C
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A;Cross-references: UNIPROT:P75520; UNIPARC:UPI0000131886;
A;Note: the nucleotide sequence was submitted to the EMBL I
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A;Genetic code: SGC3
C;Superfamily: CDPdiacylglycerol-glycerol-3-phosphate
C;Keywords: transferase
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0; Mismatches
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C; Species: Nostoc sp. PCC 7120
C; Species: Nostoc sp. PCC 7120
A; Note: Nostoc sp. PCC 7120
A; Note: Nostoc sp. Strain PCC 7120
A; Note: Nostoc sp. Strain PCC 7120
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Uul-2004
C; Accession: AE2047
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ar A; Accession: AE2047
A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Residues: 1-360 < MUR>
A; Residues: 1-360 < MUR>
A; Residues: 1-360 < MUR>
A; Experimental source: strain PCC 7120
C; Genetics:
A; Experimental source: strain PCC 7120
C; Genetics:
A; Gene: all1931
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Pred. No. 1.1e+02;
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Matches 4; Conservative
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C.)Species details succession A6943
R.Kunst. F.) Gasawara, N.; Moszer, I.; Alberini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 130, 249-256, 1997
A; Athlors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, S.; Maueel
J.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portacelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sakoin, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Scavowska, A.; Scoflan,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tanakoshi, A.; Tanamoto, H.; Yamamoto, H.; Yamamoto, K.; Yasumoto, K.; Asumoto, K.; Yasumoto, R.; Myatthors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.;
A;Reference number: A69580; MUD:98044033; PMID:9384377
A;Restreferences: UNIPROT:031597; UNIPARC:UPI0000660207; GB:299110; GB:AL009126; NID:9
A;Reperimental source: strain 168
C;Genetics:
A;Gene: YjbA
C;Superfamily: Bacillus subtilis hypothetical protein yjbA
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oligopeptide ABC transporter, permease protein - Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-J
C;Accession: G72215
C;Accession: G72215
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C
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Species: Bacillus subtilis;
Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-J
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A; Title: Evidence for lateral gene transfer between Archaea and A; Reference number: A72200; MUID: 99287316; PMID:10360571

A; Accession: G72215

A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-289 < ARN>
A; Residues: 1-289 < ARN>
A; Cross-references: UNIPROT: Q9X270; UNIPARC: UPI00000D385E; GB: AE
A; Experimental source: strain MSB8
C; Genetics:
A; Gene: TM1748
C; Superfamily: oligopeptide permease protein oppB
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Pred. No. 66;
0; Mismatches
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GB:AE006469; PIDN:AAK65021.3

Barloy-Huble: Fisher, R.F.

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Sinorhizobium melilc

Search completed: May 2, 2006, 08:56:18 Job time : 17.5116 secs

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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                    Copyright
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- protein search, using sw model OM protein May Run on:

2, 2006, 08:38:27 ; Search time 90.6047 Seconds (without alignments) 62.295 Million cell updates/sec

US-10-046-922-68 35 1 GYWXXXWX 8 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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Result No.	Score	Query Match	Length	DB	ID	Description
-	7.4	97.1	72	2	02 OR	35302 oryza sati
1 0	3.4	97.1	0	-	ML2 THIFE	88 thiobacil
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4	34	97.1	236	8	M9_9HI	9wgw9 human immu
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10	34	97.1	459	7	GV3_LAC	9kgv3 lactococc
11	34	7	464	7	84DL5	84d15 oenoc
12	34	7.	465	7	613F7_B	6i3f7 bacillus
13	34	97.1	465	7	4MN56_BAC	4mn56 bacillus c
14	34	7	465	7	81HZ7_BAC	81hz7 bacillus c
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16	34	7	465	7	6HNI4_BAC	6hni4 bacillus t
17	34	7	465	7	73DL5	73d15 bacillus
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13	34	7.	467	7	65F15_E	65£15 b
20	34	7	469	7	6TK71_	6tk71 streptoco
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22	34	7	471	7	6HP27	27 bacillus
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25	3.4	۲.	472	~	914E4_PS	914e4 pseudomona
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27	34	97.1		H	RCD LA	3092 lactobacil
28	34	97.1		7	OO PSE	4zt00 pseudomona
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31	34	7		~	88P50_PSEP	88250

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# ALIGNMENTS

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01, Created) 05, Last sequence update) 24, Last sequence update) 24, Last annotation update) 24, Last annotation update) 25, Last annotation update) 26, Last sequence update) 27, Last annotation update) 38, Streptophyta; Embryophyta 39, Liliopsida; Poales; E  Oryza.  E.B., Lyubomirskaya N.V., Na 30, Lyubomirskaya N.V., Na 32, 1483-1486 (1985) 32:1483-1486 (1985) 32:1483-1486 (1985) 33:12 gene cluster in rice mit 32; gene cluster in rice mit 33; gene cluster in rice mit 34; gene cluster in rice mit 35; gene cluster in rice mit 36; gene cluster in rice mit 36; gene cluster in rice mit 37; gene cluster in rice mit 38; gene cluster in rice mit 39; gene cluster in rice mit 30; gene cluster in rice mit	42DE53BED2 core 34; red. No. 1 Mismatcl
T. 1. 2 AA. 2015.02 ORYSA PRELIMINARY; PRT; 72 AA. 2015.302_ORYSA PRELIMINARY; PRT; 72 AA. 2015.302_ORYSA PRELIMINARY; PRT; 72 AA. 2015.302_ORYSA PRELIMINARY; PRT; 72 AA. 2015.02 ORYSA STEMBLrel. 05, Last sequence update) 01-UNA-1998 (TrEMBLrel. 24, Last annotation update ORF72B.  Oryza sativa (japonica cultivar-group).  Mitcochondrion.  Mitcochondrion.  Oryza stiva (japonica cultivar-group).  Mitcochondrion.  More TaxID=39947;  Enhartoideae; Oryzeae; Oryza.  NUCLEOTIDE SEQUENCE.  Baev A.A., Dzhumagaliev E.B., Lyubomirskaya N.V., 11' in Y.V.;  Il' in Y.V.;  Il' in Y.V.;  Dokl. Akad. Nauk SSSR 282:1483-1486 (1985).  Il' Structure of long and short copies of the mobile of Drosophila melanogaster.";  Dokl. Akad. Nauk SSSR 282:1483-1486 (1985).  Il' in Y.V.;  Il' in	; 8155 MW; 97.1%; ty 57.1%; ervative 0
Oryza china per	ENCE 7 atch cal Simi
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34 GYWSSHW 40 , Db

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EMBL; AF121641; HSSP; P03366; 1H
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01-NOV-1999
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        01-FEB-1991 (Rel. 17, Created)
13-SEP-2005 (Rel. 17, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Hypothetical 12.3 kDa protein in mobl 3'region (ORF 4).
Thiobacillus ferrooxidans.
Plasmid pTF1.
Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillales;
Acidithiobacillaceae; Acidithiobacillus.
NCBI_TaxID=920;
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MUCLECTIDE SEQUENCE.

MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;

Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,

Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,

Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,

Webb E.A., Zinser E.R., Chisholm S.W.;

"Genome divergence in two Prochlorococcus ecotypes reflects oceaniche differentiation.";

Nature 424:1042-1047(2003).

EMBL; BX572092; CAE19526.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                 restriction restriction
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95 PROMP

Q7U395.

Q7U395.

01-OCT-2003 (TrEMBLrel. 25, Created)

01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Possible Adenoviral fiber protein (Repeat/shaf).

OrderedLocusNames=PMM1067;

Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 /

Prochlorococcus correctia; Prochlorales; Prochlorococcaceae;
                                                                                                                                                                                                                                                                                                                                                                        Length 108;
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                                                                                                                                                                                Drolet M., Zanga P., Lau P.C.K.; "The mobilization and origin of transfer regions of a ferrooxidans plasmid: relatedness to plasmids RSF1010 Mol. Microbiol. 4:1381-1391(1990).
                                                                                                                                                                                                                                                                                                                                                                 DB 1; L
Lu. No. 1.8e+02;
Mismatches
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PIR; S12193; S12193.
Hypothetical protein; Plasmid.
SEQUENCE 108 AA; 12335 MW; A8E67717C1
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Pred.
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STRAIN=ATCC 33020;
MEDLINE=91125140; PubMed=2280689;
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J. virol. 73:3975-3985(1999).

EMBL; AF121641; AAD29013.1; -; Genomic_DNA.
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Wolinsky
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032816_LACLC PRELIMINARY; PRT; 253 AA.
032816;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Arginine/ornithine antiporter homolog ArcD (Fragment)
Name=arcD;
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                           update)
                                                                       Viruses; Retro-transcribing viruses; Retroviridae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
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Pred. No. 3.7e+02;
); Mismatches 3;
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MEDLINE=99214336; PubMed=10196293;
Wilson C.C., Brown R.C., Korber B.T., Wilkes
Sakamoto D., Kunstman K., Luzuriaga K., Hanso
Wiznia A., Clapp S., Ammann A.J., Koup R.A.,
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Hopwood D.A.;
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STRAIN=HTE831 / DSM 14371 / JCM 11309;

A Takami H., Takaki Y., Uchiyama I.;

Takami H., Takaki Y., Uchiyama I.;

"Genome sequence of Oceanobacillus iheyensis isolated from the Ridge and its unexpected adaptive capabilities to extreme environments.";

Nucleic Acids Res. 30:3927-3935(2002).

Nucleic Acids Res. 30:3927-3935(2002).

R GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0006810; P:transport; IEA.

GO; GO:0006810; P:transport; IEA.

R GO; GO:0006810; P:transmembrane; Transport.

R Complete proteome; Transmembrane; Transport.

SEQUENCE 294 AA; 31323 MW; F75E50F22EA4071A CRC64;
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OrderedLocusNames=OB0434;
Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus
                                                                                       by ISS1 transposition.";
J. Bacteriol. 179:4473-4479(1997).

EMBL; U81991; AAC45504.1; -; Genomic_DNA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005279; F:amino acid-polyamine transporter activity;

GO; GO:0006865; P:amino acid transport; IEA.

InterPro; IPR002293; AA/rel_permeasel.
                                               STRAIN=MG1363;
MEDLINE=97369814; PubMed=9226255;
Duwat P., Cochu A., Ehrlich S.D., Gruss A.;
"Characterization of Lactococcus lactis UV-sensitive mutants
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Pred. No. 3.9e+02;
0; Mismatches 3
                                                                                                                                                                                                         26569 MW; 1CB8FAEF6C38FBB1
 Bacteria; Firmicutes; Lactobacillales;
NCBI_TaxID=1359;
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Matches 4; Conservative
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01-MAR-2003
01-MAR-2003
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14 ACIAD QEF6U4\_ACIAD PRELIMINARY;

RESULT O6F6U4 ID O

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PubMed=15514110; DOI=10.1093/nar/gkh910;

PubMed=15514110; DOI=10.1093/nar/gkh910;

Barbe V., Vallenet D., Fonknechten N., Kreimeyer A., Oztas S.,

Labarre L., Cruveiller S., Robert C., Duprat S., Wincker P.,

Cornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;

Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;

Nucleic Acids Res. 32:5766-5779(2004).

R DDP1, a versatile and naturally transformation competent bacterium.";

Nucleic Acids Res. 32:5766-5779(2004).

R GO; GO:0016020; C:membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0006814; P:sodium ion transport; IEA.

R InterPro; IPR002657; BilAc/Na_symport.

R Pfam; PF01758; SBF; 1.

R Complete proteome.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein SCO0224.
OrderedLocusNames=SCO0224; ORFNames=SCJ9A.03c;
Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycese.
                                                              acid transporter
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STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis Gentley S.D., Chater K.P., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Cocronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Ho Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter Seeger K., Saunders D., Sharp S., Squares S., Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Par
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PIR; T37139; T37139.
Complete proteome; Hypothetical protein.
SEOUENCE 345 AA; 36929 MW; 23643009936285B8
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                                                                                                                      Acinetobacter sp. (strain ADP1).
Bacteria; Proteobacteria; Gammaproteobacteria;
Moraxellaceae; Acinetobacter.
NCBI_TaxID=62977;
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Pred. No. 5e+02;
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence up
05-JUL-2004 (TrEMBLrel. 27, Last annotation
Putative transporter; putative sodium/bile a
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Nature 417:141-147(2002).
EMBL; AL939104; CAB53264.1;
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                                                                                                       OrderedLocusNames=ACIAD3583
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Q9SIR7;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
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NCBI_TaxID=1902;
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STRAIN=ATCC 23344;

X PubMed=15377793; DOI=10.1073/pnas.0403306101;

Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,

Reldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,

Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J

Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,

Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,

Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y

Zafar N., Zhou L., Fraser C.M.;

"Structural flexibility in the Burkholderia mallei genome.";

Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).

EMBL; CP000011; AAU46467.1; -; Genomic_DNA.
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OrderedLocusNames=BMAA1038;
Burkholderia mallei (Pseudomonas mallei).
Bacteria, Proteobacteria, Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
NCBI_TaxID=1360;
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DB 2;
5.2e+02;
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STRAIN=ML3;
Chou L., Weimer B., Xie Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ
                                                                                                                451 AA
    Score 34; DB
Pred. No. 5.2e
0; Mismatches
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57.1%;
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O62C74;
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
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3 LACLA
Q9KGV3_LACLA PRELIMINARY;
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01-OCT-2000
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01-MAR-2004
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oeni genes encoding proteins
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Pred. No. 6.7e+02;
0; Mismatches 3;
Chou L.-S., Weimer B., Xie Y.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ da EMBL; AF282249; AAF86987.1; -; Genomic DNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005279; F:amino acid-polyamine transport.
GO; GO:0006865; P:amino acid transport; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR002293; AA/rel permeasel.
InterPro; IPR004841; Permease region.
Pfam; PF00324; AA permease; 1.
Transmembrane; Transport.
SEQUENCE 459 AA; 49146 MW; 9718F27B7E937242
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Pred. No. 6.8e+02;
0; Mismatches 3
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STRAIN=ATCC 23279;

MEDLINE=22519090; PubMed=12631210;

DOI=10.1046/j.1365-2672.2003.01907.x;

DOI=10.1046/j.1365-2672.2003.01907.x;

Divol B., Tonon T., Morichon S., Gindreau E., "Molecular characterization of Oenococcus oeniinvolved in arginine transport.";

J. Appl. Microbiol. 94:738-746(2003).

EMBL; AF541253; AAO83382.1; -; Genomic_DNA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0006865; P:amino acid-polyamine transport; GO; GO:0006810; P:transport; IEA.

InterPro; IPR004841; Permease_region.

InterPro; IPR004841; Permease_region.

Pfam; PF00324; AA_permease; 1.

Transmembrane; Transport.

SEQUENCE 464 AA; 50557 MW; 1C6EE79AFF9F8B8
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Bacteria; Firmicutes; Lactobacillales;
NCBI_TaxID=1247;
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Richardson P., Rubin E., Tice H.;
Richardson P., Rubin E., Tice H.;
I.Complete genome sequence of Bacillus anthracis Sterne.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
BEMBL; AE017225; AAT52924.1; -; Genomic_DNA.
R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:0016020; C:membrane; IEA.
R GO; GO:0006865; P:amino acid-polyamine transporter activity; IEA.
R GO; GO:0006865; P:amino acid transport; IEA.
R GO; GO:0006810; P:transport; IEA.
R GO; GO:0006811; P:transport; IEA.
R GO; GO:0006811; Permease.
R InterPro; IPR004841; Permease.
InterPro; IPR004841; Permease.
InterPro; IPR004841; Permease.
InterPro; IPR004841; Permease.
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PubMed=15155910; DOI=10.1073/pnas.0402414101;

PubMed=15155910; DOI=10.1073/pnas.0402414101;

Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,

Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,

Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,

Rilstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,

Rilstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,

Popovic T., Fraser C.M.;

Rilstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,

Popovic T., Fraser C.M.;

"Identification of anthrax toxin genes in a Bacillus cereus associ

with an illness resembling inhalation anthrax.";

Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).

-!- CAUTION: The sequence shown here is derived from an

EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                es; Bacillales; Bacillaceae; Bacillus;
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EMBL; AAEK01000024; EAL13575.1; -; Genomic_DNA.
SEQUENCE 465 AA; 50180 MW; F2A1540B055C90B9 CRC64;
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Pred. No. 6.8e+02;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Arginine/ornithine antiporter.
Name=arcD; ORFNames=BCE_G9241_0606;
    update)
on update
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                                                                                                                                                                                                                                                                                                                                                                                  Score 34; 'DB 2; | Pred. No. 6.8e+02; 0; Mismatches 3
                                                                                                                          NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA)
   05-JUL-2004 (TrEMBLrel. 27, Last sequence up 05-JUL-2004 (TrEMBLrel. 27, Last annotation Amino acid permease family protein. OrderedLocusNames=BAS0596;
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nembrane; Transport.
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ilarity 57.1%;
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Best Local Similarity 57.1%;
Matches 4; Conservative
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6_BACCE
04MN56_BACCE PRELIMINARY;
                                                       Bacillus anthracis.
Bacteria, Firmicutes, Bacillus cereus group.
NCBI_TaxID=1392;
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NUCLEOTIDE SEQUENCE.

MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;

Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,

Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus
Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Walunas T.,

Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,

Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
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Lucas S.
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat Arginine/ornithine antiporter.
OrderedLocusNames=BC0629;
Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacillus cereus group.
Bacillus cereus group.
NCBI_TaxID=226900;
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Hitchcock P., Jackson P., Keim P., Longmire
Richardson P., Rubin E., Tice H.;
"Complete genome sequence of Bacillus cereus
Submitted (JUL-2004) to the EMBL/GenBank/DDB
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GO; GO:0005279; F:amino acid-polyamine t
GO; GO:0006865; P:amino acid transport;
GO; GO:0006810; P:transport; IEA.
InterPro; IPR002293; AA/rel_permeasel.
InterPro; IPR004841; Permease_region.
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EMBL; AE017000; AAP07646.1; -; Genomic
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Bacteria; Firmicutes; Bacillales;
Bacillus cereus group.
NCBI_TaxID=288681;
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Pred. No. 6.8e+02;
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GO; GO:0006810; P:transport; IEA.
InterPro; IPR002293; AA/rel_permeasel.
InterPro; IPR004841; Permease_region.
Pfam; PF00324; AA_permease; 1.
Complete proteome; Transmembrane; Transport.
SEQUENCE 465 AA; 50178 MW; 55D7083AAE7B3958 CRC64;
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US-09-792-616-9

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US-09-647-140B-8

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US-09-543-681A-7620

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Sequence 1516, Ap Sequence 1516, Ap Sequence 60715, A Sequence 1191, Ap Sequence 1191, Ap Sequence 1191, Ap Sequence 1191, Ap Sequence 7633, Ap Sequence 7633, Ap Sequence 7239, Ap Sequence 5312, Ap Sequence 5312, Ap Sequence 6253, Ap Sequence 62994, A Sequence 6312, Ap Sequence 62994, A Sequence 62994, A Sequence 62994, A Sequence 62994, A	Bush CID SEQUENCES RELATING TO DIAGNOSTICS AND THERAPEUTICS ION
US-09-949-016-9656 US-09-962-756-1516 US-09-270-767-60715 US-09-082-279B-1191 US-09-315-304B-1191 US-09-315-965A-1191 US-09-350-641C-1191 US-09-350-641C-1191 US-09-621-976-7633 US-09-621-976-7633 US-09-621-976-7633 US-09-252-991A-19685 US-09-252-991A-19685 US-09-252-991A-19685 US-09-252-991A-19685 US-09-270-767-45223 US-09-489-039A-8752 US-09-712-363-168 US-09-712-363-168	LIGNMENTS  532A  ACID AND AMINO A  CCUS FAECIUM FOR  9660  own> 09/107,532A  8 051571  97  Deneke '489 : GTC-012 NN: 77
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AND THERAPEUTICS
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        Sequence 18697, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SECTITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18697
LENGTH: 543
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Pred. No. 3.1e+02;
; Mismatches 3
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n Elasticum
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Pred. No. 7.5e+02;
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US-09-792-616-9
; Sequence 9, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene enco
; TITLE OF INVENTION: Pseudoxanthoma Elasticu
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
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US-09-792-616-3
; Sequence 3, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene enc; TITLE OF INVENTION: Pseudoxanthoma Elastic; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
                                                                                                                                                                                                                                                                ; LENGTH: 543
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18697
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4; Conservat
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US-09-252-991A-23328

i Sequence 23328, Application US/09252991A

j Patent No. 6551795

j GENERAL INFORMATION:
    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING T

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING T

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING T

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING T

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 23328

LENGTH: 499
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATITIES OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
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Pred. No. 3.1e+02;
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Mismatches
               Score 34;
Pred. No.
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Pred. No.
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US-09-252-991A-19339
; Sequence 19339, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
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               Query Match
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Best Local Similarity
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APPLICANT: Bj rnvad,
APPLICANT: Clausen,
APPLICANT: Schlein,
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Best Local Similarity
Matches 4; Conser
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US-09-902-540-12675
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LENGTH: 252
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                                                                                                                                                                                                                                          US-09-64/--
Sequence 8, Applications Sequence 8, Applications Sequence 8, Applications Sequence 8, Patent No. 6803184
GENERAL INFORMATION:
APPLICANT: Fox Chase Cancer Center APPLICANT: Belinsky, Martin G. APPLICANT: Belinsky, Martin G. APPLICANT: Belinsky, Martin G. TITLE OF INVENTION: MrP-Related ABC Transporter Encorners of Invention: Nucleic Acids and Methods of U FILE REFERENCE: FCCC 98-02
CURRENT APPLICATION NUMBER: US/09/644
PRIOR PILING DATE: 1999-03-26
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-37
PRIOR FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 33
AUTHOR APPLICATION NUMBER: 60/095,153
PRIOR FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 33
ACFTWARE: FastSEQ for Windows Version 3.0
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No. 7.5e+02;
                                                                                         ore 33; DB 2; Lesd. No. 7.5e+02; Mismatches 3;
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US-09-902-540-12675

Sequence 12675, Application US/09902540

Patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Wiegand, Roger C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Seq.

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 12675

LENGTH: 88
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      SEQ ID NO 3
LENGTH: 1503
TYPE: PRT
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                                                 ; ORGANISM: H
US-09-792-616-3
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Length 88;
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2.3e+02;
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US-09-543-681A-7620;
Sequence 7620, Application US/09543681A;
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACTITLE OF INVENTION: DIAGNOSTICS AND THERAPEU;
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A;
CURRENT FILING DATE: 2000-04-05
  DB
                                   Mismatches
                    94
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Pred. No.
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APPLICANT: Schlein, Martin
APPLICANT: Schlein, Martin
APPLICANT: Stergaard, Peter Rabbek
APPLICANT: Stergaard, Peter Rabbek
APPLICANT: Sj holm, Carsten
TITLE OF INVENTION: NOVEL GALACTANASES
FILE REFERENCE: 5481.200-US
CURRENT APPLICATION NUMBER: US/09/502,653
CURRENT FILING DATE: 2000-02-11
EARLIER APPLICATION NUMBER: PA 1999 00799
EARLIER FILING DATE: 1999-06-07
EARLIER FILING DATE: 1999-03-24
EARLIER FILING DATE: 1999-03-24
EARLIER FILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No.
 Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                              60/128,706
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Clausen, Ib Groth
Schlein, Martin
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illarity 57.1%;
Conservative
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US-09-502-653-10
                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US (PRIOR FILING DATE: 1999-04-09 NUMBER OF SEQ ID NOS: 8344 SEQ ID NO 7620 LENGTH: 177
   91.4%;
57.1%;
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                                     Conservative
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2.5e+02;
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Pred. No. 2.5e+02;
; Mismatches 3;
                                  Sequence 11, Application US/09145828A

Sequence 11, Application US/09145828A

Batent No. 6403349

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories

APPLICANT: Huang, Yung-Sheng

APPLICANT: Huang, Yung-Sheng

APPLICANT: Thurmond, Jennifer

APPLICANT: Huang, Yung-Sheng

APPLICANT: Thurmond, Jennifer

APPLICANT: Huang, Yung-Sheng

APPLICANT: Huang, Yung-Shen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-09-903-456-18
is Sequence 18, Application US/09903456
j Patent No. 6677145
j GENERAL INFORMATION:
j APPLICANT: Abbott Laboratories
j APPLICANT: Huang, Yung-Sheng
j APPLICANT: Heang, Yung-Sheng
j APPLICANT: Huang, Yung-Sheng
j APPLICANT: Pereira, Suzette L.
j TITLE OF INVENTION: ELONGASE GENES AND USES THE
j FILE REFERENCE: 6407.US.P3
j CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT FILING DATE: 2001-07-11
j PRIOR APPLICATION NUMBER: US 09/624,670
j PRIOR FILING DATE: 1999-08-23
j PRIOR FILING DATE: 1999-08-23
j PRIOR FILING DATE: 1998-09-02
j NUMBER OF SEQ ID NOS: 116
software: FastSEQ for Windows Version 4.0
seq ID NO 18
j LENGTH: DATE
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Pred. No.
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US-09-624-670-17
; Sequence 17, Application US/09624670
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; ORGANISM: Caenorhabditis
US-09-903-456-18
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APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATIN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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2.4e+02;
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  Mismatches
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Patent No. 6566066

GENERAL ENFORMATION:
APPLICANT: Walker, Michael G.
APPLICANT: Volkmuth, Wayne
APPLICANT: Klinger, Tod M.
TITLE OF INVENTION: AQUAPORIN-8 VARIANT
FILE REFERENCE: PC-0012 CIP
CURRENT APPLICATION NUMBER: US/09/610,906
CURRENT FILING DATE: 2000-07-06
PRIOR FILING DATE: 1999-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
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Pred. No. 3
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PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
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US-09-248-796A-15791
; Sequence 15791, Application US/09248796A
; Patent No. 6747137
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larity 57.1%;
Conservative
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; OTHER INFORMATION: GenBank
; PUBLICATION INFORMATION:
US-09-610-906-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Candida albicans
US-09-248-796A-15791
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SOFTWARE: PERL Program
   Conservative
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LENGTH: 263
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ORGANISM:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Das, Tapas
APPLICANT: Das, Tapas
APPLICANT: Huang, Yung-Sheng
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Thurmond, Jennifer M.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407-03.P2
CURRENT APPLICATION NUMBER: US/09/624,670
CURRENT FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 278
TYPE: PRT
CREATION CARNORIES
TYPE: PRT
CREATION CAEDORIES
CORGANISM: Caenorhabditis elegans
US-09-624-670-17
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Length 278;

Score 32; DB 2; L6 Pred. No. 2.5e+02; 0; Mismatches 3;

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/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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Descript	Seque	a١	Sequenc	Sequenc	Sequence	Sequenc	Sednenc	Seguence	. Seguenc	å	Sednenc	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	a)	egu	egu	Φ	Seguenc	edn	ednen	ednen	Sequen
SUMMARIES	-115-30	-10-437-963-17603	-10-091-007-8	-10-282-122A-49	-10-369-493-2329	-282-122A-662	-10-282-122A-5280	-10-369-493-13	-10-282-122A-5768	-10-282-122A-681	-10-282-122A-5033	-09-894-018-8	-10-474-960A-	-10-046-922-3	-10-046-922-3	-10-425-115-28776	-10-425-115-2732	-09-910-483-	-48	-09-910-483-9	-09-910-483-1	-09-910-483-1	JS-09-910-483-21	-910-483-2	-910-483-2	-910-483-3	-483-3
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3 - 4 3 - 4 5 - 3 9 - 4	-10-160-23	-10-282-122A-6 -10-425-115-34	-10-450-763-4303	-10-369-493-1981	-10-369-493-165	US-10-437-963-199114	-10-450-022-	0-022-5		5B-	US-10-433-747B-2
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### ALIGNMENTS

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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Xovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                Clone ID: MRT4577_44726C.1.pep
RESULT 1
US-10-425-115-308836

US-10-425-115-308836

Sequence 308836, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La RoBa, Thomas J.

APPLICANT: La RoBa, Thomas J.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222) B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 308836

LENGTH: 58
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US-10-437-963-176036
; Sequence 176036, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 4; Conser
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US-10-425-115-308836
                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Zea mays
FEATURE:
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                                                                                                  OTHER INFORMATION: Clone ID: PAT_MRT4530_73824C.1.pep
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                                                                                                                                                   Score 34; DB 4; Losted. No. 1.5e+02; 0; Mismatches 3;
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6.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Identification of Essential FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB Pred. No. 6.4e 0; Mismatches
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                                                                                                                                                                                                                                                                                                                               Sequence 88, Application US/10091007
; Sequence 88, Application US/10091007
; Publication No. US20030170782A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics limited
; APPLICANT: Le Page, Richard W F
; APPLICANT: Hanniffy, Sean B
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21978WO
; CURRENT APPLICATION NUMBER: US/10/091,007
; CURRENT FILING DATE: 2002-03-06
; PRIOR FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 49513, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; SEQ ID NO 88
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-10-091-007-88
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Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsýth, R.
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Conservative
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Best Local Similarity 57.1%;
Matches 4; Conservative
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 176036
LENGTH: 72
                                                TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
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US-10-282-122A-49513
                                                                                                                    US-10-437-963-176036
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-10-091-007-88
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APPLICANT:
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Sequence 23291, Application US/10369493
; Sequence 23291, Application US/20030233675A1
; Sequence 23291, Application No. US20030233675A1
; Publication No. US20030233675A1
; APPLICANT: Cao, Yongwei
; APPLICANT: Blatc, Greven C.
; APPLICANT: Gldman, Barry S.
; APPLICANT: Gldman, Barry S.
; APPLICANT: Gldman, Barry S.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US 60/360,039
; RIOR APPLICATION NUMBER: US 60/360,039
; RIOR APPLICATION NUMBER: US 60/360,039
; RIOR APPLICATION STATE 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 23291
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6.6e+02;
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US-10-282-122A-66258
; Sequence 66258, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
          R FILING DATE: 2000-05-26

R APPLICATION NUMBER: 60/230,335

R FILING DATE: 2000-09-06

R APPLICATION NUMBER: 60/230,347

R FILING DATE: 2000-09-09

R APPLICATION NUMBER: 60/242,578

R FILING DATE: 2000-10-23

R APPLICATION NUMBER: 60/253,625

R FILING DATE: 2000-11-27

R APPLICATION NUMBER: 60/257,931

R FILING DATE: 2000-12-22

R FILING DATE: 2000-12-22

R FILING DATE: 2001-02-09

R FILING DATE: 2001-02-09

R APPLICATION NUMBER: 60/267,636

R APPLICATION NUMBER: 60/267,636
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 49513
LENGTH: 466
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                                                                                                                                                                                                                                                                       anisms
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APPLICANT: Foreyth, R.
APPLICANT: Foreyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION Identification of Essential Genes in Microorganism TITLE OF INVENTION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-07
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Pred. No. 6.7e+02;
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; Sequence 52805, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
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Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Wang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
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Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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Carr, Grant
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ENGTH: 472
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TITLE OF I
FILE REFER
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                        APPLICANT :
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Sequence 13733, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Gldman, Barry S.

APPLICANT: Gldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFEINS IN

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 13733

LENGTH: 475
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Pred. No. 6.7e+02
; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   removed
CURRENT APPLICATION NUMBER: US/10/282, CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21 PRIOR FILING DATE: 2000-05-23 PRIOR APPLICATION NUMBER: 60/207,727 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-09-06 PRIOR FILING DATE: 2000-09-06 PRIOR FILING DATE: 2000-09-06
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R APPLICATION NUMBER: 60/242,578

R FILING DATE: 2000-10-23

R FILING DATE: 2000-11-27

R FILING DATE: 2000-11-27

R APPLICATION NUMBER: 60/257,931

R FILING DATE: 2000-12-22

R FILING DATE: 2000-12-22

R APPLICATION NUMBER: 60/267,636
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APPLICATION NUMBER: 60/269,308
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US-10-369-493-13733
                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application data
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 52805
LENGTH: 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Clostridium botulinum-10-282-122A-52805
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US-10-369-493-13733
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ITTLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 PRIOR FILING DATE: 2007 PRIOR FILING DATE: 2007 PRIOR FILING DATE: 2007 PRIOR APPLICATION NUMBER: 60/191 070 PRIOR FILING DATE: 2007 070 PRIOR APPLICATION NUMBER: 60/191 070 PRIOR APPLICATION NUMBER: 60/191
                                                                          Essential Genes in Microorganisms
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5.7e+02;
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2003-02-20
ER: 60/191,078
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Pred. No.
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Sequence 50338, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
                                    APPLICANT: FOISYCH, K.
APPLICANT: YU, H.
TITLE OF INVENTION: Identification of E
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,1
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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OR FILING DATE: 2000-03-21
OR FILING DATE: 2000-05-23
OR APPLICATION NUMBER: 60/207,727
OR FILING DATE: 2000-05-26
OR APPLICATION NUMBER: 60/207,727
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Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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57.1%;
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US-10-282-122A-68169
Robert
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lio, Carlos
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EQ ID NO 68169
LENGTH: 475
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Zamudio, Carlo
Malone, Cheryl
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6.7e+02;
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TITLE OF INVENTION: Identification of Essenti
FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: 60/191,078

PRIOR PILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR APPLICATION NUMBER: 60/267,636
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Pred. No. 6.7e
0; Mismatches
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Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 57680
RESULT 9
US-10-282-122A-57680
; Sequence 57680, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
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                                                                                                                                              wang, bransar
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
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US-10-282-122A-68169
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Sequence 87, Application US/10474960A

Sequence 87, Application US/10474960A

Publication No. US20040248113A1

GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Brown, David
TITLE OF INVENTION: Methods and System for Optimizing Multi-epitope Nucleic
TITLE OF INVENTION: Acid Constructs and Peptides Encoded Thereby
FILE REFERENCE: 2060.0320004
TITLE OF INVENTION: Methods and System for Optimizing Multi-epitope Nucleic
TITLE OF INVENTION: Methods and System for Optimizing Multi-epitope Nucleic
TITLE OF INVENTION: Mark
APPLICANT: Acid Constructs and Peptides Encoded Thereby
FILE REFERENCE: 2006.0320004
CURRENT APPLICATION NUMBER: US/10/474,960A
CURRENT PILING DATE: 2003-01-06
PRIOR FILING DATE: 2001-06-27
PRIOR PELICATION NUMBER: US 60/284,221
PRIOR APPLICATION NUMBER: US 60/284,221
PRIOR FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Koivunen, Erkki
APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATI
FILE REFERENCE: 28967/37084A
CURRENT APPLICATION NUMBER: US/10/046,922
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Pred. No.
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Publication No. US20020164667A1
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn version
SEQ ID NO 34
LENGTH: 10
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                  US-10-474-960A-87; Sequence 87, App.; Publication No.
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SOFTWARE: Fa
SEQ ID NO 87
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iS Sequence 87, Application US/09894018

iS Sequence 87, Application US/09894018

iS Patent No. US20020119127A1

GENERAL INFORMATION:

APPLICANT: EPIMMUNE, Inc.,
APPLICANT: Chestnut, Robert
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Baker, Denisw
APPLICANT: Baker, Denisw
APPLICANT: Baker, Denisw
APPLICANT: Brown, David
TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING
TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
FILE REFERENCE: 39963-20033.00
CURRENT APPLICATION NUMBER: US/09/894,018
CURRENT APPLICATION NUMBER: PRIOR FILING DATE: 2001-12-28

PRIOR FILING DATE: 2001-12-28

PRIOR FILING DATE: 2001-04-16

NUMBER OF SEQ ID NOS: 368

SOFTWARE: FastSEQ for Windows Version 4.0
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7e+02;
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Pred. No. 7e+0
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PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-09
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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ilarity 57.1%;
Conservative
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Sequence 35, Application US/10046922
Sequence 35, Application US/10046922
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 28967/37084A
CURRENT APPLICATION NUMBER: US/10/046,922
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 35
LENGTH: 10
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US-10-995-561-968

US-10-467-657-5906

US-11-079-463-8428

US-11-079-463-7586

US-11-079-463-10025

US-11-079-463-10025

US-11-079-463-10025

US-11-079-463-10025

US-11-079-463-10025

US-11-079-463-10025

US-11-087-099-7125

US-11-087-099-7125

US-11-045-024-4377

US-11-045-024-4377

US-11-045-024-4500

US-11-045-024-263

US-11-045-024-263

US-11-045-024-6641

US-11-045-024-6570

US-11-045-024-6641

US-11-045-024-6641

US-11-045-024-6130
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US-11-087-099-11321
; Sequence 11321, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plan; FILE REFERENCE: 38-21 (53450) B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 11321
; LENGTH: 469
Sequence 1003, Application US/11087099; Publication No. US20060041961A1; GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plar; FILE REFERENCE: 38-21(53450) B EP; CURRENT APPLICATION NUMBER: US/11/087,099; CURRENT FILING DATE: 2005-03-22; NUMBER OF SEQ ID NOS: 12464; SEQ ID NO 1003; LENGTH: 464
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US-11-087-099-2298
; Sequence 2298, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 2298
; LENGTH: 475
                                                                                         Score 34; DB pred. No. 92; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB Pred. No. 92; 0; Mismatches
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US-11-087-099-7571

Sequence 7571, Application US/11087099

Publication No. US20060041961A1

GENERAL INFORMATION:

APPLICANT: Abad, Mark S. et al.

TITLE OF INVENTION: Genes and Uses for Plant

FILE REFERENCE: 38-21(53450)B EP

CURRENT APPLICATION NUMBER: US/11/087,099

CURRENT FILING DATE: 2005-03-22

NUMBER OF SEQ ID NOS: 12464

SEQ ID NO 7571

LENGTH: 475
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; Sequence 6764, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
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                                                Pseudomonas syringae pv. -1870
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US-11-087-099-7571
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4; Conservative
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; SEQ ID NO 18
; LENGTH: 47
; TYPE: PRT
; ORGANISM:
US-11-087-099-
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TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
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                                                                                                                                                     Sequence 19864, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 19864
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US-11-087-099-1870
; Sequence 1870, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
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US-11-087-099-12291
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Score 34; DB
Pred. No. 92;
0; Mismatches
                       US-11-087-099-9555.
US-11-087-099-9555.
Sequence 9555, Application US/11087099;
Publication No. US20060041961A1;
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for F;
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,09;
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464;
SEQ ID NO 9555;
                                                                                                                                                                                        ORGANISM: Clostridium perfringens str.
-11-087-099-9555
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ilarity 57.1%;
Conservative
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TITLE OF INVENTION: Genes and Uses for Plant FILE REFERENCE: 38-21(53450)B EP CURRENT APPLICATION NUMBER: US/11/087,099 CURRENT FILING DATE: 2005-03-22 NUMBER OF SEQ ID NOS: 12464 LENGTH: 478
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   PLANT
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Mismatches
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APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant; FILE REFERENCE: 38-21(53450)B EP; CURRENT APPLICATION NUMBER: US/11/087,099; CURRENT FILING DATE: 2005-03-22; NUMBER OF SEQ ID NOS: 12464; SEQ ID NO 1256; LENGTH: 476
; FILE REFERENCE: 38-21(53452)B; CURRENT APPLICATION NUMBER: US/11/188,298; CURRENT FILING DATE: 2005-07-22; PRIOR APPLICATION NUMBER: 60/592,978; PRIOR FILING DATE: 2004-07-31; NUMBER OF SEQ ID NOS: 22569; SEQ ID NO 6764; LENGTH: 475
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Pred. No.
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Pred. No.
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Pred. No.
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; Sequence 7019, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Clostridium perfringens
US-11-087-099-1256
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US-11-087-099-7019
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US-11-188-298-6764
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APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant; FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099; CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464; SEQ ID NO 4146; LENGTH: 482
                                                                                                                                                                                                                                                                                                                                                                                               Score 34;
Pred. No.
                                                                                                                                                                    US/11/188,298
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RESULT 12
US-11-188-298-8872
US-11-188-298-8872; Application US/11188298; Sequence 8872, Application US/11188298; Publication No. US20060075522A1; GENERAL INFORMATION:
TITLE OF INVENTION: GENES AND USES FOR FILLE REFERENCE: 38-21(53452)B; CURRENT APPLICATION NUMBER: US/11/188,29; CURRENT FILING DATE: 2005-07-22; PRIOR APPLICATION NUMBER: 60/592,978; PRIOR FILING DATE: 2004-07-31; NUMBER OF SEQ ID NOS: 22569; SEQ ID NO 8872; LENGTH: 478
                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Clostridium perfringens str. US-11-188-298-8872
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US-11-087-099-4146
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US-11-250-411-97
Sequence 97, Application US/11250411
Publication No. US20060034838A1
GENERAL INFORMATION:
APPLICANT: TTO, MIKITO
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: NAKAMDA, YOKO
APPLICANT: NAKAMDA, YOKO
APPLICANT: NAKAMDA, WASABUMI
TILE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTI-FILE OF INVENTION: ANDER: US/11/250,411
CURRENT APPLICATION NUMBER: US/11/250,411
CURRENT APPLICATION NUMBER: US/11/250,411
CURRENT APPLICATION NUMBER: US/09/453,718
PRIOR APPLICATION NUMBER: 09/315,051
PRIOR APPLICATION NUMBER: 09/119,014
PRIOR APPLICATION NUMBER: 09/119,014
PRIOR APPLICATION NUMBER: PCT/JP97/04259
PRIOR APPLICATION NUMBER: DS/11-21
SOFTWARE: PATENTING DATE: 1998-07-20
PRIOR APPLICATION NUMBER: DS/11-21
SEQ ID NO 97
LENGTH: 119
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CRGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Description of Artificial Sequence:
US-11-250-411-97
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US-11-087-099-9097
; Sequence 9097, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Imp;
FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9097
; LENGTH: 491
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Mismatches
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Pred. No. 5
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Pred. No.
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US-11-087-099-9097
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Similarity 57.1%; 4; Conservative
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